

XX

PI Tang YT, Liu C, Dirmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wehrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
DR N-PSDB: AAK52210.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PI useful in diagnosis and gene therapy -
PS Claim 20; Page 4074-4075; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
XX
SQ Sequence 477 AA;

Query Match 99.6%; Score 2471; DB 22; Length 477;
Best Local Similarity 99.6%; Pred. No. 1.8e-217;
Matches 475; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 1 MRRLRDLFPTAAACODAPRTRETLRQALDNRGCVYDICELOGSLNLTGPIGQDAE 60
DB 1 MRLVRLDVLPLAACQDAEPQPMYELLIGALDNGDVVDELGEGLNLTGPIGQDAE 60
OY 61 EKFTTGVNKKDKGLDFEEMFKYLYKDKHEKMKLAFFSKLDKNDNGKLEASEIYOSLDTGL 120
DB 61 EKFTTGVNKKDKGLDFEEMFKYLYKDKHEKMKLAFFSKLDKNDNGKLEASEIYOSLDTGL 120
OY 121 TISEQDAELILOSIDVGTMTVDMNEMRDYFLFNPVTIDIEIRFKKSHSTGIDIGSLT 180
DB 121 TISEQDAELILOSIDVGTMTVDMNEMRDYFLFNPVTIDIEIRFKKSHSTGIDIGSLT 180
OY 181 PDEFDEKSSGOWMROLLAGIAGAVSRTAPLDRLKIMQVHGSKSDKXNIFEGFRO 240
DB 181 PDEFDEKSSGOWMROLLAGIAGAVSRTAPLDRLKIMQVHGSKSDKXNIFEGFRO 240
OY 241 MVEEGGIRSLMNGNTNVIKIPETAFAVKEAYEYKRLTEBQKIGTFEPISSGMA 300
DB 241 MVEEGGIRSLMNGNTNVIKIPETAFAVKEAYEYKRLTEBQKIGTFEPISSGMA 300
OY 301 TQOTFTYPMWKTTRAVKKTQYSIYDCAKKILKHEGLGAFYKGYVNLGIYRAGI 360
DB 301 TQOTFTYPMWKTTRAVKKTQYSIYDCAKKILKHEGLGAFYKGYVNLGIYRAGI 360
OY 361 DIAYVELKSYMLDNFAKXSVNPGVWVLICGALSTCGOLSTPYALVTRTRQAAME 420
DB 361 DIAYVELKSYMLDNFAKXSVNPGVWVLICGALSTCGOLSTPYALVTRTRQAAME 420
OY 421 GSPQLMVGILFRRIISKEGIPGLYRGITPNEFMKLVPAVGISYVYVBNMKOTLGVTOK 477
DB 421 GSPQLMVGILFRRIISKEGIPGLYRGITPNEFMKLVPAVGISYVYVBNMKOTLGVTOK 477

RESULT 2
AAU27697
ID AAU27697 standard; Protein; 471 AA.
XX
XX AAU27697;
XX

DT 18-DEC-2001 (first entry)
XX
XX Human full-length polypeptide sequence #22.
DE
XX Mammal: human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
KW nervous system disorder; inflammatory disorder; cell differentiation;
KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;
KW cytoskeletal; antirheumatic; antiarthritic; vulnery; antiinflammatory;
KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
KW neuroprotective; osteoprotic; antidiabetic; antiallergic;
KW immunostimulant; analgesic; gene therapy.
XX
XX Homo sapiens.
PN WO200164834-A2.
PD
PD 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US04926.
XX
XX 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
PR 17-JUN-2000; 2000US-0597707.
PR 14-JUL-2000; 2000US-0616807.
PR 19-SEP-2000; 2000US-0664641.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
PI Dirmanac R;
XX
XX WPI: 2001-589862/66.
DR N-PSDB: AAS44597.
XX
XX Novel polypeptides and nucleic acids obtained from cDNA libraries
PT prepared from various human tissues, for diagnosis, treatment of
PT cancer, neurological, inflammatory disorders and for use in arrays for
PT detection -
XX
XX Claim 10; SEQ ID NO 194; 153pp; English.
PS
XX Sequences AAU27676-AAU28019 represent full-length polypeptides and
CC contig polypeptides of the invention. The proteins and their associated
CC DNA sequences are useful for the treatment, diagnosis and prevention of
CC various types of disorder in a mammalian subject such as a human, dog,
CC monkey, mouse, hamster or rat. The disorders include cancers such as
CC leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as
CC multiple sclerosis, connective tissue disease, rheumatoid arthritis,
CC diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
CC disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
CC chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
CC Werner's disease, inflammatory disorders such as nephritis, Crohn's
CC disease, ischemia-reperfusion injury, shock, sepsis and inflammatory
CC bowel disease. The sequences exhibit activity relating to angiogenesis,
CC cell proliferation, cell differentiation, stem cell growth factor,
CC activin or inhibin. Therefore, they can be used to manipulate stem cells
CC in culture to give rise to neuroepithelial cells that can be used to
CC augment or replace cells damaged by illness, accidental damage or genetic
CC disorders. The sequences may also be used for regeneration of bone,
CC cartilage, tendons and ligaments and in tissue repair and burn healing.
CC Note: Some sequences for this patent did not form part of the printed
CC specification, but were obtained in electronic format directly from WIRO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 471 AA;

Query Match 62.6%; Score 1552.5; DB 22; Length 471;
Best Local Similarity 61.5%; Pred. No. 2.3e-133;

Matches 286; Conservative 85; Mismatches 87; Indels 7; Gaps 2;	
OY 17	DAEOPTRRETFLFOALDRNGDGVNDIGELQEGRLNIGLPGD----AEKIFTTGDVVKD 72
Db 7	daerrtgrwgrlfeeldsnkdgrvdvhelrgrlarlg---ggnpdpqaqgissegdaddp 63
OY 73	GKLDPEEFEMKYLKDHKKMKLAFKSLDKNNDKITEASEIVSLQTLGTLTISEQOAEILIQ 132
Db 64	ggldeefsrlylgereqlllmfnsldrngghidvseiqsfraigsislegaeakllh 123
OY 133	SIDVDGWTVDWNEWRDYELFNPVTDIEITIRFKMHSSTGIDIGSLTIPDEFTDEKKS 192
Db 124	smrdgtmldwgewrdfllhslenvedvlyfwkhsfvldlgecltyvdefskqekltg 183
OY 193	QMWROLLAGGAGVAVSRSTAPLRKIMMOVHGSKSDKNMIFGGRQVMVEGGIRSLMR 252
Db 184	mmwqglvavagavavstgtctapdrllvfmqvhasktmrlllgllismvlegglsrswr 243
OY 253	GNGTNVKIKIAPETAVKFWAEQYKRLTDEGOKIGTERFISGSAGATAQTFYPMPEVM 312
Db 244	gnglnvnlkiapesaikfmayeqikrallggqetlhvgerfvaagslagataqtlilymvev 303
OY 313	KTRIAVGKTGOYSIYDCAKKILKHBGLGAFYKGYVPMNLGIIYPAGIDLAAYELLASYW 372
Db 304	ktlrlttrtgqykglllccarrllleregpralryglpvnlgldlyagldlavetclkmw 363
OY 373	LDNFAKDSVNGVWVLGGCGLSTGCGIASYPLALVTRTMOAAMLEGSPQLMWGLFR 432
Db 364	lqgshsadsdpgllvllacgllstscqglasypalavrtcmqaaaslegpqjsmlgllr 423
OY 433	RIISKEGIPGLYRGITPNFMKFLPAPVAGISYVVENMKOTLGVTOK 477
Db 424	hllsqegmrglyrgjapofmkvlpavsisyvvenmkqalgvtar 468
RESULT 3	
AAU27869 standard; Protein: 509 AA.	
AAU27869;	
18-DEC-2001 (first entry)	
Human contig polypeptide sequence #22.	
Mammal: human; rhesus monkey; baker's yeast; fission yeast; Norway rat; mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia; cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation; nervous system disorder; inflammatory disorder; cell differentiation; angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn; genetic disorder; bone regeneration; tendon; ligament; tissue repair; cytostatic; antineoplastic; antidiabetic; vulnery; antiinflammatory; antibacterial; immunosuppressive; vasotropic; antiparkinsonian; neuroprotective; osteopathic; antidiabetic; antidiabetic; antiallergic; immunostimulant; analgesic; gene therapy.	
Homo sapiens.	
Synthetic.	
WO200164834-A2.	
07-SEP-2001.	
26-FEB-2001, 2001WO-US04926.	
28-FEB-2000, 2000US-0515126.	
18-MAY-2000, 2000US-0577409.	
17-JUN-2000, 2000US-0597707.	
14-JUL-2000, 2000US-0616807.	
19-SEP-2000, 2000US-0664641.	
(HYSE-) HYSEQ INC.	

PI	Tang YF, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F, Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C; Drmanic R;
PI	WPI: 2001-589862/66.
DR	N-PSDB: AAS44769.
XX	
PT	Novel polypeptides and nucleic acids obtained from cDNA libraries prepared from various human tissues, for diagnosis, treatment of cancer, neurological, inflammatory disorders and for use in arrays for detection
PT	Claim 10; Page 126-127; 153pp; English.
PS	
XX	
CC	Sequences AAU27676-AAU28019 represent full-length polypeptides and contig polypeptides of the invention. The proteins and their associated DNA sequences are useful for the treatment, diagnosis and prevention of various types of disorder in a mammalian subject such as a human, dog, monkey, mouse, hamster or rat. The disorders include cancers such as leukaemia, lymphoma and neuroblastoma, autoimmune disorders such as multiple sclerosis, connective tissue disease, rheumatoid arthritis, diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system disorders such as Parkinson's disease, Alzheimer's disease, Huntington's chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and Werner's disease, inflammatory disorders such as nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis and inflammatory bowel disease. The sequences exhibit activity relating to angiogenesis, cell proliferation, cell differentiation, stem cell growth factor, activin or inhibin. Therefore, they can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, accidental damage or genetic disorders. The sequences may also be used for regeneration of bone, cartilage, tendons and ligaments and in tissue repair and burn healing.
CC	Note: Some sequences for this patent did not form part of the printed specification, but were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
CC	
XX	
SO	Sequence 509 AA;
Query Match 62.6%; Score 1552.5; DB 22; Length 509;	
Best Local Similarity 61.5%; Pred. No. 2.6e-133;	
Matches 286; Conservative 85; Mismatches 87; Indels 7; Gaps 2;	
OY 17	DAEOPTRRETFLFOALDRNGDGVNDIGELQEGRLNIGLPGD----AEKIFTTGDVVKD 72
Db 45	daerrtgrwgrlfeeldsnkdgrvdvhelrgrlarlg---ggnpdpqaqgissegdaddp 101
OY 73	GKLDPEEFEMKYLKDHKKMKLAFKSLDKNNDKITEASEIVSLQTLGTLTISEQOAEILIQ 132
Db 102	ggldeefsrlylgereqlllmfnsldrngghidvseiqsfraigsislegaeakllh 161
OY 133	SIDVDGWTVDWNEWRDYELFNPVTDIEITIRFKMHSSTGIDIGSLTIPDEFTDEKKS 192
Db 162	smrdgtmldwgewrdfllhslenvedvlyfwkhsfvldlgecltyvdefskqekltg 221
OY 193	QMWROLLAGGAGVAVSRSTAPLRKIMMOVHGSKSDKNMIFGGRQVMVEGGIRSLMR 252
Db 222	mmwqglvavagavavstgtctapdrllvfmqvhasktmrlllgllismvlegglsrswr 281
OY 253	GNGTNVKIKIAPETAVKFWAEQYKRLTDEGOKIGTERFISGSAGATAQTFYPMPEVM 312
Db 282	gnglnvnlkiapesaikfmayeqikrallggqetlhvgerfvaagslagataqtlilymvev 341
OY 313	KTRIAVGKTGOYSIYDCAKKILKHBGLGAFYKGYVPMNLGIIYPAGIDLAAYELLASYW 372
Db 342	ktlrlttrtgqykglllccarrllleregpralryglpvnlgldlyagldlavetclkmw 401
OY 373	LDNFAKDSVNGVWVLGGCGLSTGCGIASYPLALVTRTMOAAMLEGSPQLMWGLFR 432
Db 402	lqgshsadsdpgllvllacgllstscqglasypalavrtcmqaaaslegpqjsmlgllr 461
OY 433	RIISKEGIPGLYRGITPNFMKFLPAPVAGISYVVENMKOTLGVTOK 477

DB	462	h1sgcgmrglyg1apn1mkvlpavsisywyemkqalgytst	506
RESULT	4		
ID	AA66718		
XX	AA66718 standard; protein; 469 AA.		
XX			
AC	AA66718;		
XX			
DT	05-APR-2000 (first entry)		
XX			
DE	Membrane-bound protein PRO1106.		
XX			
KW	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;		
KX	pharmaceutical; receptor Immunoadhesin; gene mapping.		
XX			
OS	Homo sapiens.		
XX			
PN	WC9963088-A2.		
XX			
PD	09-DEC-1999.		
XX			
PF	02-JUN-1999;	99WO-0512252.	
XX			
PR	02-JUN-1998;	98US-0087607.	
PR	02-JUN-1998;	98US-0087609.	
PR	02-JUN-1998;	98US-0087759.	
PR	03-JUN-1998;	98US-0087827.	
PR	04-JUN-1998;	98US-0088021.	
PR	04-JUN-1998;	98US-0088025.	
PR	04-JUN-1998;	98US-0088028.	
PR	04-JUN-1998;	98US-0088029.	
PR	04-JUN-1998;	98US-0088030.	
PR	04-JUN-1998;	98US-0088033.	
PR	04-JUN-1998;	98US-0088326.	
PR	05-JUN-1998;	98US-0088167.	
PR	05-JUN-1998;	98US-0088202.	
PR	05-JUN-1998;	98US-0088212.	
PR	05-JUN-1998;	98US-0088217.	
PR	09-JUN-1998;	98US-0088655.	
PR	10-JUN-1998;	98US-0088722.	
PR	10-JUN-1998;	98US-0088730.	
PR	10-JUN-1998;	98US-0088734.	
PR	10-JUN-1998;	98US-0088738.	
PR	10-JUN-1998;	98US-0088740.	
PR	10-JUN-1998;	98US-0088741.	
PR	10-JUN-1998;	98US-0088742.	
PR	10-JUN-1998;	98US-0088810.	
PR	10-JUN-1998;	98US-0088811.	
PR	10-JUN-1998;	98US-0088824.	
PR	10-JUN-1998;	98US-0088825.	
PR	10-JUN-1998;	98US-0088826.	
PR	11-JUN-1998;	98US-0088858.	
PR	11-JUN-1998;	98US-0088861.	
PR	11-JUN-1998;	98US-0088863.	
PR	11-JUN-1998;	98US-0088866.	
PR	12-JUN-1998;	98US-0088876.	
PR	12-JUN-1998;	98US-0089090.	
PR	12-JUN-1998;	98US-0089105.	
PR	16-JUN-1998;	98US-0089440.	
PR	16-JUN-1998;	98US-0089512.	
PR	16-JUN-1998;	98US-0089514.	
PR	17-JUN-1998;	98US-0089532.	
PR	17-JUN-1998;	98US-0089538.	
PR	17-JUN-1998;	98US-0089598.	
PR	17-JUN-1998;	98US-0089599.	
PR	17-JUN-1998;	98US-0089600.	
PR	17-JUN-1998;	98US-0089653.	
PR	18-JUN-1998;	98US-0089601.	
PR	18-JUN-1998;	98US-0089907.	
PR	18-JUN-1998;	98US-0089908.	
PR	19-JUN-1998;	98US-0089947.	
PR	19-JUN-1998;	98US-0089948.	

[illegible]

XX 27-MAR-2000 (first entry)
DE Murine ADR/ATP transporter family protein, SEQ ID NO:339.
KW Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
KW embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
KW secreted; transmembrane; inflammation; cancer; neurological disease;
KW angiogenesis; tumor vascularisation; growth disorder;
KW developmental disorder; skin wound; hair follicle disorder;
KW anti-inflammatory; cytosolic; neuroprotective; vulnery.
XX Mus sp.
XX WO955865-A1.
XX 04-NOV-1999.
XX 29-APR-1999; 99WO-NZ00051.
XX 29-APR-1998; 98US-0069726.
XX 09-NOV-1998; 98US-0188930.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;
XX WPI: 2000-072177/06.
XX N-PSDB: AA61789.
XX Novel polynucleotides useful for the treatment of various conditions
XX including wounds and cancer -
XX
XX Claim 4; Page 199-200; 235pp; English.
XX
XX The invention relates to novel nucleic acid sequences derived from rat
XX dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
XX and mouse embryonic skin, keratinocyte stem cells and transit amplifying
XX cells. Polypeptides of the invention may be used to treat inflammation,
XX cancer and neurological diseases. The proteins may be used to stimulate
XX the growth and motility of keratinocytes, to inhibit the growth of
XX cancer cells, to modulate angiogenesis and tumour vascularisation, to
XX inhibit skin inflammation, to modulate epithelial cell growth and to
XX inhibit binding of HIV-1 to leukocytes. The invention may also be used
XX to treat growth and developmental defects, skin wounds and hair follicle
XX disorders. Sequences AA75942-Y76123 represent polypeptides encoded
XX by cDNA sequences derived from several mouse, rat or human skin cell
XX types. Sequences AA75942-Y75947, AA76020-Y76021, AA76094-Y76104 and
XX AA76119 are proteins with an N-terminal signal sequence, indicating
XX that they are secreted. Sequences AA75986-Y75989, AA76061-Y76071,
XX AA76106-Y76109 and AA76121-Y76122 are proteins with one or more
XX putative transmembrane domains.
XX
XX Sequence 469 AA:
SQ

Query Match 60.4%; Score 1499; DB 21; Length 469;
Best Local Similarity 65.6%; Pred. No.1,8e-128;
Matches 274; Conservative 73; Mismatches 71; Indels 0; Gaps 0;

QY 60 EEKIFTTGDNVNDKGLDFEFEMKYLKDHEKMKLAFLSKDKNNDGKTEASEIVSIQTITG 119
DB 52 kqklvqagdkldqgldfdeefvhyqdhcklrlvfkskldkndgldqelmsqldrdy 111
QY 120 LTIISQQAALLIQTSDVDTMTVDNNEKRDYFLFNPTVITIEELIRKWKSTGIDIDISLT 179
DB 112 vrlseagaeiklismoknglmtidnewrdyhlhpvenipellilywkhtlfdvgent 171
QY 180 IPDEFTEDEKSGGOMROLLAGIAGAVSRTSTAPDLRLKIMMVGSKSDKMNINGGR 239
DB 172 vpdelfteerqvgmwrhlvvaagsgavsrctclapdlrlkvlmqvnaasnmncivgft 231
QY 240 OMVKBEGSIRSLMRNGTGNVIAKETAVKFWAYEYKLLTEEGQKIGFERFISGMAG 299

DB 232 qmlreggakselwrgnglnvklipesaiklmayqgmrlvgsdgelrlherlvagslag 291
QY 300 ATAQTFFYPMWEVMAKTRILAVKCTGOYSGIYDCAKIKLKHGIGAFYKGVVNLGIIPYAG 359
DB 292 alqsgslypmvevlktrmalrkktqsgmlcdarrllakegvaelykypimlgiipyag 351
QY 360 IDLAVVELLSYMLDNPFAKSVNPGVWVLLGCGALSTCGOLASPLAVTRMQAOAML 419
DB 352 ldlavvelkntwldqrvavnsadpgvrvllacgltscgqlasplavtrmqagasi 411
QY 420 EGSPOLMMVGLFRRIRISKEGIPGLYRGITPEFMKVLPAVGISVYVYENMKQTIGVTK 477
DB 412 egapevemsstfkqglrtcgafglyrslapnfmkvlpavsisyvvynlklitgvqsr 469

RESULT 8
AAB56023
ID AAB56023 standard; Protein; 469 AA.
XX
AC AAB56023;
XX
DT 08-MAR-2001 (first entry)
XX
DE Skin cell protein, SEQ ID NO: 339.
XX
KW Mouse; skin cell; cytosolic; antiinflammatory; anti-HIV;
KW nootropic; neuroprotective; vulnery; immunomodulatory; vaccine;
KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;
KW inflammation; neurological disease.
XX
OS Mus sp.
XX
XX WO200069884-A2.
XX
XX 23-NOV-2000.
XX
XX 15-MAY-2000; 2000WO-NZ00075.
XX
XX 14-MAY-1999; 99US-0312283.
XX
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX
XX Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;
XX WPI: 2001-007495/01.
XX N-PSDB: AAC99722, AAC99806.
XX
XX New isolated polynucleotide used in the identification of genetic
XX disorders and encoding polypeptides used for treating inflammatory
XX disease, cancer and neurological diseases -
XX
XX Claim 4; Page 266-267; 352pp; English.
XX
XX The present sequence is a polypeptide which is expressed in
XX mammalian skin cells. The polypeptide is useful for stimulating
XX keratinocyte growth and motility, inhibiting the growth of cancer cells,
XX modulating angiogenesis, inhibiting angiogenesis and vascularisation of
XX tumours, modulating skin inflammation, stimulating the growth of
XX epithelial cells, inhibiting the binding of human immunodeficiency virus
XX (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
XX neurological diseases. The polynucleotide can be used as a marker, in
XX the identification of genetic disorders, and for the design of
XX oligonucleotides for examining expression patterns.
XX
XX Sequence 469 AA:
SQ

Query Match 60.4%; Score 1499; DB 22; Length 469;
Best Local Similarity 65.6%; Pred. No.1,8e-128;
Matches 274; Conservative 73; Mismatches 71; Indels 0; Gaps 0;

QY 60 EEKIFTTGDNVNDKGLDFEFEMKYLKDHEKMKLAFLSKDKNNDGKTEASEIVSIQTITG 119

DB 52 kqkivagqdkaldgldfeefvhyiqdhekkirlyfksldkknqgridageimsgslrdlg 111
QY 120 LTIISQOQELLISQIDVOSTMTVDNENMDYFLFNPVDIEELIFPKHSTGIDIGDSLT 179
DB 112 vliisqgaekllksmdkngtcmldmewdyhllnpvenlillywksltfdvgentl 171
QY 180 IPDEFTEDEKSSGOWMROLIAGIAGAVSRSTAPLDRILKIMOVHSGSKSDKMNIFGGR 239
DB 172 vpdeltveerqgmwrhvlvaggagavsrctctaptdrilkmqyhasrsmnmcilvgftl 231
QY 240 OMVKGSGIRSLRNGSTNVIKIAPETAVKFMAYEOYKLLTEGOKIGFEFFRISGNAG 299
DB 222 qmtrgsgaksrlwrginglnvkliapesalklmageqmkrlvgsdqetlrlherlrvagslag 291
QY 300 ATAQETIYPMEMVKTRLAVAGKTGYSGIYDCAKIILKHEGLAFKGYVNPMLGITIPYAG 359
DB 232 alagesslypmeyklrmlalrktcgysgmldcarrllakegvaafkgyipmnlglipyag 351
QY 360 IDLAYELKSYWLDNFADSVNPGVMILGCGALSTGQSLASYPALVTRTMOAOAML 419
DB 332 idlayetlknwldgrvavnsadpgvfvlacgtlssctgqlasypalvtrtmqagast 411
QY 420 EESPOLNMVGLFRRITISKEGIPGLYRGITPNNPKVLPANGISYVYVENMKOTLGYTOK 477
DB 412 egapevtsmslftqllrtlegafglyrjlapnfmkvipavsisyvvenlklclgyvqr 469

RESULT 9
ABG22637
ID ABG22637 standard; Protein; 508 AA.
XX AC ABG22637;
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #22628.
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
OS Homo sapiens.
PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PE 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Dmanac RT, Liu C, Tang YT;
XX DR WPI; 2001-639362/73.
XX DR N-PSDB; AAS86824.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity -
PS Claim 20; SEQ ID NO 52996; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX SQ Sequence 508 AA;

Query Match 59.6%; Score 1479.5; DB 22; Length 508;
Best Local Similarity 59.3%; Pred. No. 1.3e-126;
Matches 277; Conservative 85; Mismatches 96; Indels 9; Gaps 4;

QY 17 DAEQPTRETLFOALDRNGDGVYDIGELQEGRLNIGLPGOD---AEEKITTTGDKND 72
DB 45 deerrqwrgrlleeidsnkdgrvdvdelrqlarlg---ggnpdpqagqgssegdapn 101
QY 73 GKLDPEEFKYLKDEHKMKMLAFKSLDNKNDKIPASEIVOSLQTLGLTISQOQEL-IL 131
DB 102 gglidleeefrylqereqrlmlfhdldrngdghlvselsqgsfralgslllegckhfa 161
QY 132 QSIDVDGTTWTVDMNEMRDVLEFNPVYDIEIRFKHSTGIDIGSLTIPDEFTEDEKS 191
DB 162 gavdrqgmldwgwrdfllhslenvedvlyfkwstvidigecltvpdefskqeklt 221
QY 192 GOWMROLIAGIAGAVSRSTAPLDRILKIMOVHSGSKSDKMNIFGFGOMVMEGIRSLW 251
DB 222 gmmwqkqagavagavsrqgtpvlidrlkvfmqvhasknrlnllgllsmvlegjrlslw 281
QY 252 RQNGTNNVIKIAPETAVKFMAYEOYKLLTEGOKIGFEFFRISGMAGATAQTFIYPMEV 311
DB 282 rgnjnlvkliapesalklmageqikrpalpgeketlrvlerfagslagatqillymew 341
QY 312 MKTRLAVGRTQYSGIYDCAK-KILKHGCLAFYGYVNPMLGITIPYAGIDLAVTELKS 370
DB 342 lktlrltrtgqykglaqlrgrllereqprafyglpvnvlgllpyagidlavetlkn 401
QY 371 VWLDNFADSVNPGVMILGCGALSTGQSLASYPALVTRTMOAOAMEGSPOLNMVGL 430
DB 402 wvlqgysnhsadpgllvlacgtlssctgqlasypalvtrtmqagastegqklsmlgll 461
QY 431 FRRITISKEGIPGLYRGITPNNPKVLPANGISYVYVENMKOTLGYTOK 477
DB 462 lrhlisqegmrglyrjlapnfmkvipavsisyvvenlklclgyvqr 508

RESULT 10
AAB42329
ID AAB42329 standard; Protein; 385 AA.
XX AC AAB42329;
XX DT 08-FEB-2001 (first entry)
XX DE Human ORFX ORF2093 polypeptide sequence SEQ ID NO:4186.
XX KM Human; open reading frame; ORFX; detection; cytosstatic; hepatotropic;
XX KM vulnereary; antiporiatric; antiparkinsonian; nootropic; neuroprotective;
XX KM anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
XX KM immunostimulant; thrombolytic; coagulant; vasocortic; antidiabetic;
XX KM hypotensive; dermatological; immunosuppressive; antiinflammatory;
XX KM antiviral; antibacterial; antifungal; antihematic; antihyroid;
XX KM antianemic; gene therapy; cancer; proliferative disorder; hypertension;
XX KM neurodegenerative disorder; osteoarthritis; graft vs host disease;

PR	01-SEP-2000	2000US-02293343
PR	01-SEP-2000	2000US-02293345
PR	01-SEP-2000	2000US-02293346
PR	05-SEP-2000	2000US-02295109
PR	05-SEP-2000	2000US-02295153
PR	06-SEP-2000	2000US-02304337
PR	06-SEP-2000	2000US-02304348
PR	08-SEP-2000	2000US-02312422
PR	08-SEP-2000	2000US-02312424
PR	08-SEP-2000	2000US-02312443
PR	08-SEP-2000	2000US-02314113
PR	08-SEP-2000	2000US-02314114
PR	08-SEP-2000	2000US-02320801
PR	12-SEP-2000	2000US-02320860
PR	12-SEP-2000	2000US-02319688
PR	14-SEP-2000	2000US-02322397
PR	14-SEP-2000	2000US-02323398
PR	14-SEP-2000	2000US-02323409
PR	14-SEP-2000	2000US-02323460
PR	14-SEP-2000	2000US-02323461
PR	14-SEP-2000	2000US-02330633
PR	14-SEP-2000	2000US-02330634
PR	14-SEP-2000	2000US-02330637
PR	21-SEP-2000	2000US-02343223
PR	21-SEP-2000	2000US-02343225
PR	21-SEP-2000	2000US-02344297
PR	25-SEP-2000	2000US-02344974
PR	25-SEP-2000	2000US-02344998
PR	26-SEP-2000	2000US-02354844
PR	27-SEP-2000	2000US-02358334
PR	27-SEP-2000	2000US-02358336
PR	29-SEP-2000	2000US-02363227
PR	29-SEP-2000	2000US-02363567
PR	29-SEP-2000	2000US-02363568
PR	29-SEP-2000	2000US-02363569
PR	29-SEP-2000	2000US-02363593
PR	29-SEP-2000	2000US-02363602
PR	02-OCT-2000	2000US-02363602
PR	02-OCT-2000	2000US-02370337
PR	02-OCT-2000	2000US-02370338
PR	02-OCT-2000	2000US-02370339
PR	02-OCT-2000	2000US-02370340
PR	13-OCT-2000	2000US-02393935
PR	13-OCT-2000	2000US-02393937
PR	20-OCT-2000	2000US-02409560
PR	20-OCT-2000	2000US-02411821
PR	20-OCT-2000	2000US-02411825
PR	20-OCT-2000	2000US-02417867
PR	20-OCT-2000	2000US-02417876
PR	20-OCT-2000	2000US-02418078
PR	20-OCT-2000	2000US-02418084
PR	20-OCT-2000	2000US-02418109
PR	01-NOV-2000	2000US-02446177
PR	08-NOV-2000	2000US-02446474
PR	08-NOV-2000	2000US-02446475
PR	08-NOV-2000	2000US-02446476
PR	08-NOV-2000	2000US-02446476
PR	08-NOV-2000	2000US-02446477
PR	08-NOV-2000	2000US-02464778
PR	08-NOV-2000	2000US-02465223
PR	08-NOV-2000	2000US-02465229
PR	08-NOV-2000	2000US-02465639
PR	08-NOV-2000	2000US-02466110
PR	08-NOV-2000	2000US-02466111
PR	08-NOV-2000	2000US-02466113
PR	08-NOV-2000	2000US-02466127
PR	17-NOV-2000	2000US-02492508
PR	17-NOV-2000	2000US-02492507
PR	17-NOV-2000	2000US-02492510
PR	17-NOV-2000	2000US-02492519
PR	17-NOV-2000	2000US-02493911

PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250391.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI; 2001-488781/53.
DR N-PSDB; AA163830.
XX
XX
PT New isolated nucleic acids and polypeptides, useful for diagnosing,
PT treating and/or preventing human diseases and disorders -
XX
XX
PS Claim 11; SEQ ID NO 202; 664pp + Sequence Listing; English.
XX
XX
CC The invention relates to human polynucleotides (AA163803-AA164012) and
CC the encoded proteins (AA1643497-AA1643660) useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer,
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX
SQ Sequence 244 AA:

Query Match 46.1%; Score 1143; DB 22; Length 244;
Best Local Similarity 94.8%; Pred. No. 2.7e-96;
Matches 219; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 MRLWLDPLPRAACDAQPPRTRETLFQALDRNGGVVDIGELGSLNKLPIPLGDAE 60
DB 14 MLRWLDPLPRAACDAQPPRTRETLFQALDRNGGVVDIGELGSLNKLPIPLGDAE 73
QY 61 EKIFTTGVDNRKQKGLDFEEMFKYLRKDEKKMKLAFKSLDKNNNGKTEASEIYOSLTGL 120
DB 74 EKIFTTGVDNRKQKGLDFEEMFKYLRKDEKKMKLAFKSLDKNNNGKTEASEIYOSLTGL 133

QY 121 TISEQAEILLIISIDVDGTMVDMNEMWRDYFLFNPTVDIEIIRKKSHTGIDIGSLTI 180
DB 134 TISEQAEILLIISIDVDGTMVDMNEMWRDYFLFNPTVDIEIIRKKSHTGIDIGSLTI 193
QY 181 PDFFTEDEKSSGQWWRQLLAGGIVASRTSTAPIDRLKIMQVHGSKSDK 231
DB 194 pdfftedekssgqwwrqlilagivagaxststapldrlkimqvsgnqtk 244
RESULT 14
AA19941
ID AA19941 standard; Protein; 244 AA.
XX
XX AA19941;
AC
XX
DT 06-DEC-2001 (first entry)
XX
XX
DE Novel human calcium-binding protein #50.
XX
XX
KW Human; calcium-binding protein; calcium flux; neurological disease;
KW immune dysfunction; digestive disorder; neoplastic disease;
KW blood disorder; infectious disease; gene therapy; immunosuppressive;
KW antarthritic; cytostatic; vasotropic; antibacterial; nootropic;
KW virucide.
XX
XX
OS Homo sapiens.
XX
XX
PN WO20015304-A2.
XX
PD 02-AUG-2001.
XX
XX
PF 17-JAN-2001; 2001WO-US01302.
XX
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227189.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.

PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234423.
PR 21-SEP-2000; 2000US-0234424.
PR 25-SEP-2000; 2000US-023497.
PR 25-SEP-2000; 2000US-023498.
PR 25-SEP-2000; 2000US-023498.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.

PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465568/50.
DR N-PSDB; AAS31626.
XX
PT Isolated nucleic acid molecule encoding a calcium-binding protein is
XX used in preventing, treating or ameliorating a medical condition
XX
PS Claim 11; SEQ ID No 138; 542pp; English.
XX
XX The present invention relates to the isolation of novel human
CC calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic
CC sequences encoding for these proteins. The sequences of the invention
CC are useful in the diagnosis, prevention and/or prognosis of diseases
CC associated with aberrant calcium flux. Such disorders include
CC neurological diseases (e.g. amyotrophic lateral sclerosis, ALS),
CC immune dysfunction (e.g. severe combined immunodeficiency, SCID),
CC digestive disorders (e.g. irritable bowel syndrome, IBS), neoplastic
CC disease (e.g. cancer), blood disorders (e.g. haemophilia), and/or
CC infectious disease (e.g. acquired immunodeficiency syndrome, AIDS). The
CC novel calcium-binding proteins are also useful as screening tools to
CC identify antagonists and/or agonists that may enhance or inhibit
CC activities mediated by calcium-binding proteins. The polynucleotides of
CC the invention are also useful in gene therapy. AAU19892-AAU19969
CC represent the novel human calcium-binding proteins.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 244 AA:

Query Match 46.1%; Score 1143; DB 22; Length 244;
Best local similarity 94.8%; Pred. No. 2,7e-96;
Matches 219; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 MRLRLDFALPTAACDABPTREYTLFOALDRGDSVVGELQEGLRNLTGPIGDDAE 60
DB 14 MLRLDFALPTAACDABPTREYTLFOALDRGDSVVGELQEGLRNLTGPIGDDAE 73
QY 61 EKIFTTGDNKDKLDLFEEREMKYLKDEKKMKLAFKSLDRNNDGKIRASEIYVSLQTLGL 120
DB 74 EKIFTTGDNKDKLDLFEEREMKYLKDEKKMKLAFKSLDRNNDGKIRASEIYVSLQTLGL 133
QY 121 TISEQDAELILOSIDVDGNTFTVDMENEMKDYFLNPVPTDIEELIFKWKHSGIDIGDSLTT 180
DB 134 TISEQDAELILOSIDVDGNTFTVDMENEMKDYFLNPVPTDIEELIFKWKHSGIDIGDSLTT 193

QY 181 PDEFEDEKSGQWWRQLLAGIAGAVSRTSTAPLDRLKIMQVHGSKSDK 231
 |||||
 Db 194 pdefedeksgqwrqllagiagaxstxtpdrlkimvgvqngtk 244

RESULT 15

AA050388
 ID AAB50388 standard; Protein; 292 AA.

AC AAB50388;

DT 12-MAR-2001 (first entry)

DE Human uncoupling protein #11.

KW Human; uncoupling protein; immunosuppressive; antiarthritic;
 KW antirheumatic; antiproliferative; cardiant; vasotropic;
 KW cerebroprotective; neuroprotective, antibacterial; ophthalmological;
 KW gastrointestinal; nephrotropic; gynaecological; vulnary; thrombolytic;
 KW gene therapy; cancer; wound; infectious disease; thrombosis; arthritis;
 KW infertility.

OS Homo sapiens.

PN WO200061614-A2.

PD 19-OCT-2000.

PE 06-APR-2000; 2000WO-US09534.

PR 09-APR-1999; 99US-0128701.

PR 08-JUL-1999; 99US-0142821.

PR 18-AUG-1999; 99US-0149448.

PR 12-NOV-1999; 99US-0164751.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, NI J, Komatsoulis G, Rosen CA, Soppet DR;

XX WPI: 2000-656322/63.

XX N-PSDB: AAC90462.

PT Uncoupling proteins and nucleic acid sequences encoding them, useful
 PT for detecting, preventing and treating proliferative, neurological,
 PT immune system, cardiovascular and gastrointestinal disorders -

PS Claim 11; Page 328-329; 343pp; English.

CC The present sequence is a human uncoupling protein. The nucleotide
 CC sequences encoding the uncoupling proteins may be used for
 CC the detection of various disorders such as cancer, for chromosome
 CC identification, as chromosome markers and for numerous other diagnostic
 CC or research purposes. The uncoupling protein encoded by the nucleotide
 CC sequences may be used to treat disorders such as neural, immune,
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 CC renal and proliferative disorders, wounds, infectious diseases,
 CC thrombosis, arthritis, and infertility.

XX Sequence 292 AA;

Query Match 41.8%; Score 1037; DB 21; Length 292;

Best Local Similarity 65.1%; Pred. No. 1.8e-86;

Matches 181; Conservative 53; Mismatches 44; Indels 0; Gaps 0;

QY 140 MIVDNNERNRDYFLFNPVDIEIIFWFKHSTGIDIGDSLTIPDEFEDEKSGQWWRQLL 199
 |||||
 Db 1 mldidgewwrhllhlslenvedvlyfwkxstvidgecltypdetskqklgmwkkqlv 60

QY 200 AGGIGAVSRTSTAPLDRLKIMQVHGSKSDKNIEGGFROMVWKEGIRSLRGNGTNYI 259
 |||||
 Db 61 agavagavsrctapldrlkimvgvqngtknlnllygltismvlegltislrwnglnvl 120

QY 260 KIAPEYAVKFWAYEQYKLLTEEGOKIGTFERFISGSMAGATAPFIYPMYMKTRLAVG 319
 |||||
 Db 121 kiapesalkfmayeqikrallgqgetlhvgerfvagslagataqcliypmeylkrilclr 180

QY 320 KTGQYSGIYDCAKRIKHEGLGAFYKGYVPNLGIIPFAGIDLAYELKSTWLDNFAKD 379
 :|||
 Db 181 rtgqykjlldcarrieregprafyrylpmvlgilpygidlavetlknwlgqshd 240

QY 380 SVNPGVMVLLGCGALSTCGOLASYPALVPTRMQOA 417
 | :|||
 Db 241 sadpgilvllaegtlisstcgiasypalvtrmqaga 278

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 08:14:06 ; Search time 24.71 Seconds
(without alignments)
471.510 Million cell updates/sec

Title: US-09-777-921A-2
Perfect score: 2481
Sequence: 1 MLRWLRDFALEPTACQDAEQ.....VGISYVYENKQRTLGVTOK 477

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1499	60.4	469	US-09-188-930-339	Sequence 339, App
2	910	36.7	312	US-09-188-930-142	Sequence 142, App
3	347	14.0	298	US-08-961-871-10	Sequence 10, Appl
4	323.5	13.0	328	US-09-068-140A-15	Sequence 15, Appl
5	311.5	12.6	289	US-09-068-140A-10	Sequence 10, Appl
6	295	11.9	320	US-08-933-750C-12	Sequence 12, Appl
7	295	11.9	320	US-09-234-613-12	Sequence 12, Appl
8	281	11.3	674	US-09-160-119-2	Sequence 12, Appl
9	269.5	10.9	447	US-09-160-119-4	Sequence 2, Appl
10	255	10.3	351	US-08-933-750C-19	Sequence 19, Appl
11	255	10.3	351	US-09-234-613-19	Sequence 19, Appl
12	239.5	9.7	311	US-08-775-009-33	Sequence 32, Appl
13	233.5	9.4	299	US-08-518-878B-56	Sequence 56, Appl
14	233.5	9.4	299	US-08-470-868A-56	Sequence 56, Appl
15	233.5	9.4	309	US-08-518-878B-51	Sequence 51, Appl
16	233.5	9.4	309	US-08-807-861A-51	Sequence 51, Appl
17	233.5	9.4	309	US-08-470-868A-51	Sequence 51, Appl
18	233.5	9.4	309	US-09-210-681-51	Sequence 51, Appl
19	233.5	9.4	309	US-08-946-719A-51	Sequence 37, Appl
20	233.5	9.4	311	US-08-775-009-33	Sequence 37, Appl
21	229	9.2	312	US-09-142-565-2	Sequence 33, Appl
22	228	9.2	432	US-08-937-466-4	Sequence 2, Appl
23	228	9.2	432	US-09-172-528-4	Sequence 4, Appl
24	228	9.2	432	US-09-318-199-4	Sequence 4, Appl
25	228	9.2	432	US-09-503-579-4	Sequence 4, Appl
26	226	9.1	306	PCT-US94-09799-1	Sequence 1, Appl
27	224	9.0	308	US-08-937-466-2	Sequence 2, Appl

28	224	9.0	308	US-09-172-528-2	Sequence 2, Appl
29	224	9.0	308	US-09-318-199-2	Sequence 2, Appl
30	224	9.0	308	US-09-503-579-2	Sequence 2, Appl
31	198.5	8.0	303	US-08-518-878B-37	Sequence 37, Appl
32	198.5	8.0	303	US-08-294-522B-36	Sequence 36, Appl
33	198.5	8.0	303	US-08-807-861A-37	Sequence 37, Appl
34	198.5	8.0	303	US-08-470-868A-37	Sequence 37, Appl
35	198.5	8.0	303	US-09-210-681-37	Sequence 37, Appl
36	198.5	8.0	303	US-08-946-719A-37	Sequence 37, Appl
37	193.5	7.8	307	US-08-807-861A-56	Sequence 56, Appl
38	193.5	7.8	307	US-09-210-681-56	Sequence 56, Appl
39	193.5	7.8	307	US-08-946-719A-56	Sequence 56, Appl
40	186	7.5	125	US-08-905-223-320	Sequence 320, App
41	179	7.2	256	US-08-937-466-6	Sequence 6, Appl
42	179	7.2	256	US-09-172-528-6	Sequence 6, Appl
43	179	7.2	256	US-09-318-199-6	Sequence 6, Appl
44	179	7.2	256	US-09-503-579-6	Sequence 6, Appl
45	178	7.2	149	US-08-100-874-2	Sequence 2, Appl

ALIGNMENTS

```
RESULT 1
US-09-188-930-339
; Sequence 339, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Morrison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 339
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Mouse
US-09-188-930-339

Query Match      60.4%; Score 1499; DB 4; Length 469;
Best Local Similarity 65.6%; Pred. No. 5.5e-138;
Matches 274; Conservative 73; Mismatches 71; Indels 0; Gaps 0;

QY 60 EEKIFTTGDNKDGKIDFEEMKYLLKDHKKMLAKRSLDKNNDKGKIEASIVQSLOTLG 119
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 52 KOKIVAGSKDLDGQDFFEEFVHYLDHEKKRLVPSLKKNDGRDAOEIMQSLRDLG 111

QY 120 LRTSEQAELLTGSIDVDGTMVDMNEMRDYFLFNPTDIEELIRRMKSHSTGIDIDSLT 179
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 112 VKTSEQAELIKLSMDKNGMTIDNMENRDYHLHPVENLPETILTLWKSHSTIDVGENLT 171

QY 180 IPDEFTEDEKSSGOMWROLLAGSIAGAVSRTSTAPDLRLKIMQVHSGSKSDKNINIGCFR 239
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 172 VPDEFVEERQGTMMWRHLVAGGAGVSRCTCAPDLRLKLVLMQVHASSRNNNCIYGGFT 231

QY 240 QMKREGISLWNGNGNTNVIKIAPEYAVKFAWEYQTKLLTEGQKIGTFERRISGSMAG 299
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 232 OMIREGAGKSLWNGNINVLKIPESAKIFMAVEQMKRLGVSQDETLLRIHERLVAGSLAG 291

QY 300 ATQQTQTYIPREYVKTRVLAVGKTGOYSGIYCAKKILKHGIGAFYKGYVNNLIGIIPYAG 359
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
DB 292 ATRQSSITPREYVKTRMALRKTQYISGMDCARRILAKESVAFAFYGIIPNMIGIIPYAG 351

QY 360 IDLAVYELKSWLDNFANDSVNPGYVVLGCGALSTGQQLASYPDLAVTRFMQAOAML 419
   :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
```

DB 352 IDLAVYETLKNLTWLORYAVNSADPGVFNLLACGTTISSTGOLASYPALVTRMOQAASI 411
QY 420 EGGPOLNMVGLPFRRIISKEGIPGLRGITPNNFMKVLPAVGISYVYENKOTLGVTOK 477
DB 412 EGAPEYTHMSLTKQILRTGAGLIRGLAPNFMKVIPIANISIVYENKILTLGQSR 469

RESULT 2
US-09-188-930-142

; Sequence 142, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 142
; LENGTH: 312
; TYPE: PRT
; ORGANISM: mouse
US-09-188-930-142

Query Match 36.7%; Score 910; DB 4; Length 312;
Best Local Similarity 63.2%; Pred. No. 1e-80;
Matches 165; Conservative 51; Mismatches 45; Indels 0; Gaps 0;

QY 60 EKIITGVDYKDKGLDPEEPKYLKQHEKKKLAFKSIDKNNQKIEKSELYOSLOTIG 119
DB 52 KQKIYQAGKDLQDLQDFEEFVHYLDQHEKKLRLVFKSLDKKNDRIQAOEIMOSLRDG 111
QY 120 LTISSQAEILQSIDVQDVTVDNMMNDVFLFNPVTDIEETIRPFWKSTGIDIGSLT 179
DB 112 VAISQQAELIKSKDKNKTMTIIDNNEMRDYLLHRLHVEWIPILLIKWKTIFDVGENTL 171
QY 180 IPDEFTEDKSKGQWROLLAGIAGAVSRSTAPLDRILKIMQVHSGSKDKMNIJGGR 239
DB 172 VDEFTVEERQGTMMWRHLVAGGAGAVSRCTAPLDRILKIMQVHSGSKDKMNIJGGR 231
QY 240 QMVRGGGIRSLRNGTINIKIAPETAVKFAVEQYKRLTEGOKIGTFEFGISGMA 299
DB 232 QMIRGGGASLIRNGINVLKIAPESAIKEMAYEQMKRLVGSQDFTLRHERLVAAGSLAG 291
QY 300 ATAQFTIYPMVAKTRLAGVK 320
DB 292 AIAQSSIYPMVAKTRMALRK 312

RESULT 3
US-08-961-871-10

; Sequence 10, Application US/08961871
; Patent No. 6013858
; GENERAL INFORMATION:
; APPLICANT: Wallace, Douglas C.
; APPLICANT: Graham, Brett H.
; APPLICANT: Macgregor, Grant R.
; TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
; TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Mannattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US

; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 60/030,017

FILING DATE: 01-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: Feiber, Donna M.

REGISTRATION NUMBER: 33,878

REFERENCE/DOCKET NUMBER: 78-96

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 499-8080

TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 298 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-961-871-10

Query Match 14.0%; Score 347; DB 3; Length 298;
Best Local Similarity 32.2%; Pred. No. 1e-25;
Matches 95; Conservative 58; Mismatches 114; Indels 28; Gaps 10;

QY 196 ROLLGAGIAGAVSRSTAPLDRILKIMQV-HGSK---SDKM--NIEGGRQVKEGGIRS 249
DB 10 KDFLGGIAGAAVSKTAVAFIERVKLLDYOQASQISAEKQKGIIDCVRIKPKQGFIS 69
QY 250 IWRNGTINIKIAPETAVKFAVEQYKRLTEGOKIGTFEFGISGM---AGATAQT 304
DB 70 FWRGNLANVIRFEPQALNFAFKDKYKQIFLGVDNRHQQFWRYFAGNLASGAGATSLC 129
QY 305 FIYPEVAKTRLA--VGKSG---QYSGIYDCAKRLIKHGLGAFKGYVNNLGLITIPAG 359
DB 130 FVYPLDFARTTLAADVQKSSQGRFENGJLDCITKIFKSDGLGLYQGFVSVOGIITRYA 189
QY 360 IDLAVYELLKSYWLDNFAKDSVNPVWVLLGCGALSTGOLASYPALVTRMOQAAML 419
DB 190 AFEQYIDTK-----GMLPDKNVHIIYSMTAOSVTAVAGLVSPFDVRRRRMMQSGR 244
QY 420 EGGPOL--NMVGLPFRRIISKEGIPGLRGITPNNFMKVLPAVGISY--VYENMKQ 470
DB 245 KGADIMYTGTLDCWKRKIAKDEGANAFKGAWSN---VLKMGCAVLVLVYDEIKK 296

RESULT 4
US-09-068-140A-15

; Sequence 15, Application US/09068140A
; Patent No. 6281409
; GENERAL INFORMATION:
; APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor
; APPLICANT: and Rex Michael Brennan
; TITLE OF INVENTION: Blackcurrant Promoters and Genes
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,140A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: No. 6281409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Dimer, Data L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C70237
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5017
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Ribes nigrum
STRAIN: Ben Alder
US-09-068-140A-15
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```
Query Match 13.0%; Score 323.5; DB 4; Length 328;
Best Local Similarity 29.7%; Pred. No. 2.3e-23;
Matches 85; Conservative 53; Mismatches 131; Indels 17; Gaps 6;
```

```
QY 193 OMWROLLAGIAGAVSRTPAPDLRLKIMWQVHSGSKDKNNINGFRQ---NWKGGIR 248
DB 35 QFMQFIASISIASIHMAHYPTDTLKTROGIGSCSAQS---AGLRQALGSLKVEGPA 91
QY 249 SLWRNGTIVIKIAPETAFAVKEAYEQYKLLTEEGOKIGTFERRISGSMAATQFTYIP 308
DB 92 GLYRGIGAGMLGAPAHAYVESYEMCKETFS-HGDPNSGAHAYSGVFATVASDAVITP 150
QY 309 MEPMKRLAVGTGQYSGITDCAKILKHEGLGAFYKGVNPLGIIPYAGIDLAVYELL 368
DB 151 MDVVKQRLQ-LQSSPYKGVDCVRVLEEGIGAFYASRTYIVVMNAPFAVHFATYEAT 209
QY 369 KSVILNFKKDSVNPVWVLLGCGALSTCGOLASYPLALVTRMQAOAM-----LEGSP 423
DB 210 KKGLEVESEPTANDENLHVHTAGAAAGALAAVITPDLVVKIQDCCGCGCDRFSSES 269
QY 424 QLMWGLFRRISKEGIPGLYRGITPNEFKVLPVAVGISVYVENMK 469
DB 270 IDVDIG---SIVKKNKYGLMRGWIPIRMLEFHPAAALICMSTYEASK 312
```

```
RESULT 5
US-09-068-140A-10
; Sequence 10, Application US/09068140A
; Patent No. 6281409
```

```
GENERAL INFORMATION:
APPLICANT: Mary Rose Woodhead, Mark Andrew Taylor
APPLICANT: and Rex Michael Brennan
TITLE OF INVENTION: Blackcurrant Promoters and Genes
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
```

```
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,140A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/04807
FILING DATE: No. 6281409ember 4, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Dimer, Data L.
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: C70237
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5017
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Ribes nigrum
STRAIN: Ben Alder
US-09-068-140A-10
```

```
Query Match 12.6%; Score 311.5; DB 4; Length 289;
Best Local Similarity 29.5%; Pred. No. 2.8e-22;
Matches 83; Conservative 51; Mismatches 130; Indels 17; Gaps 6;
```

```
QY 198 LLAGIAGAVSRTPAPDLRLKIMWQVHSGSKDKNNIFGFRQ---MVEGGIRSLMRG 253
DB 1 MINGSLAGSIEMHAMYPDTLKTROIAGISCSAQS---AGLRQALGSLKVEGAGLYRG 57
QY 254 NGTNVIKIAPETAFAVKEAYEQYKLLTEEGOKIGTFERRISGSMAATQFTYIPMEVMK 313
DB 58 IGAMGIGAGPAHAYVESYEMCKETFS-HGDPNSGAHAYSGVFATVASDAVITPMDVVK 116
QY 314 TRLAVGTGQYSGITDCAKILKHEGLGAFYKGVNPLGIIPYAGIDLAVYELLKSYWL 373
DB 117 QRLQ-LQSSPYKGVDCVRVLEEGIGAFYASRTYIVVMNAPFAVHFATYEATKKGGL 175
QY 374 DNFADKSVNPVWVLLGCGALSTCGOLASYPLALVTRMQAOAM-----LEGSPQIMV 428
DB 176 EVSEPTANDENLHVHTAGAAAGALAAVITPDLVVKIQDCCGCGCDRFSSESIDVI 235
QY 429 GLFRRISKEGIPGLYRGITPNEFKVLPVAVGISVYVENMK 469
DB 236 G---SIVKKNKYGLMRGWIPIRMLEFHPAAALICMSTYEASK 273
```

```
RESULT 6
US-08-933-750C-12
; Sequence 12, Application US/08933750C
; Patent No. 5932442
```

```
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
```


[illegible]

	Query Match	11.3%:	Score 281:	DB 4:	Length 674;	
	Best Local Similarity	23.3%:	Pred. No. 1.le-18;			
	Matches	121;	Conservative	90;	Mismatches 221;	Indels 88; Gaps 18
QY	28	FOALDRNDGDVVDIGELØE--GLRNL--GIPRGDAEEKIPTGDVNKDGK-LDPEEFM	81			
		: : : : : : : : : : : : : :				
Db	96	FOLFDKAGKEVFEDVAQVFGQTIIHQHIFPNMOSE--FQJLHFGRKRKHLLYAETT	152			
		: : : : : : : : : : : : : :				
QY	82	KYLADHE-KKKKLAKSLDKNNKGKIEASEIYQSLOT-----GLTIS	123			
		: : : : : : : : : : : : : : : : : : : :				
Db	153	QFLLEIOLEHAQOAEVQGDNRNARTGVTAIDFREDIVITIRPHVLTEPVECLYAAAGTTIS	212			
		: : : : : : : : : : : : : : : : : : : :				
OY	124	EQ-----QAEILIOSLDVDGTMTVDNMENMDYLT-----FNPTDIIEILR	164			
		: : : : : : : : : : : : :				
Db	213	HQVSFTYNGNSLSLNNEMLIKRTISTLAGTRKRDDEVTKEEFLAQAOKFGVATPMEDVTL	272			
		: : : : : : : : : : : : :				
OY	165	FW-----KHSNGIDIG----DSLTIIPBEFTDEDK-SGQWWRQLD-----	199			
		: : : : : : : : : : : : :				
Db	273	FQDLADLYPERGRMILTIERIAPLEEGTLPFLILAQAQSGDSARPVLYQVAESARYRG	332			
		: : : : : : : : : : : : :				
QY	200	AGGIAGAVSRSTAPLDRKLTIMOVHGSKSDKM-----NIFGFRÖMYKEGINSIWMRG	253			
		: : : : : : : : : : : : : : : : : : : :				
Db	333	LGSVAGAAGAAVVPIDIVYTRMQHORSTGTSFVGELAMKNSEDCCKKYLRVGEFGIAYRG	392			
		: : : : : : : : : : : : : : : : : : : :				
OY	254	NGTNVIKIAPEFAVMFAVEYEQKILLTEBGOXIGIFFERFISSMGATAQTITYMEVWK	313			
		: : : : : : : : : : : : : : : : : : : :				
Db	393	LLPOLLGAPERAIKLIYNDVFRDKFMHKDGSVPLAETLLAGGGSOVIFTNPLETEYK	452			
		: : : : : : : : : : : : :				
QY	314	TRLAVGKTGGQY-SGIYDCAKKILKHEHGGAFFKGYVPNLGIITPRAGIDLAYELLKSVM	372			
		: : : : : : : : : : : : :				
Db	453	IRLOY--AGELTITGRYSALSIVRDLRGFFGIYKGAACAFELRPISAITFYPCYAHKA--	508			
		: : : : : : : : : : : : :				
QY	373	LDNPAKD--SVNPGVAVMLIGCGAUSSTGCQLASYPALAVYTRMQAOAMLEGGSPÖINMGL	430			
		: : : : : : : : : : : : : : : : :				
Db	509	--SFANEDGQVSPGSLLL--AGAIIGMPAASITVPADVATIKTRLOVAAAARGQTYSVIDC	564			
		: : : : : : : : : : : : :				
OY	431	ERRIISKEGIPGLRGITPPIPFMKVLPANVISVYVENMKQ	470			
		: : : : : : : : : : : : :				
Db	565	FRTIUREGPALMWAGARVRSSPOGVQVITLYELLOR	604			
		: : : : : : : : : : : : :				

```

RESULT      9
US-09-160-119-4
; Sequence 4, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRILL, ANTOINE.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 447
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-160-119-4

Query Match      10.9%; Score 269.5; DB 4; Length 447;
Best Local Similarity 23.6%; Pred No. 7,3e-18;
Matches 93; Conservative 75; Mismatches 167; Indels 59; Gaps 12

```

```

Query Match Statistics      10.9% ; Score 269.5; DB 4; Length 447;
Best Local Similarity     23.6% ; Pred. No. 7,3e-18;
Matches    93; Conservative   75; Mismatches 167; Indels   59; Gaps   12.

QY 103 DKEIEASEIVOSLQITGLTISEQAELLQSIDV---DGTMTVDWNENWRDYELFNPVTDI 159
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 17 DVEATKKEEFVLAAQKFG-QVTPMEVDILFLQADLYEPRGRMT-----LADI 61
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 160 EEIIRFMKHSTGIDIGDSITIPDETE---DEKKSGQWTKROLL-----AGTAG 205
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 ERIAPL-----EGGTLFPNLAEARQAKASGSARSAPLLLOVAESAYRFGISGVAG 111
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 206 AVSRFTSLPDLRLKIMMOVHGSKSDKM-----NIFGGFRMWKEGISTLRNGNTNY 259
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 112 AVGAIAAVYPIDLVKTRMQNRKSTSGSVGEHMKRNKSFDCKKVLRRGFFGLRGILLPLL 171
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 260 KIAPEYAVKFMAVEQYKKLTLEEGOKIGTFERFISGMAGATAQTFTFYPMYEKTRLAVG 319
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 172 GVAPRKAIKLTVFNVDVRDKFMHKDGDSVPLAIELLAGCGAGSQVIFTNPLEIVKIRLQV- 230
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 320 KTGOV-SGIYDCARKIKLNHEGLGARYYKGVPNLLGITPRAGIDLAVYELLKSYMWDNPAK 378
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 231 -AGEITTPRVSALESVNDLDFEGGYIKYKAKACFLNDIPPSALTYPCYAHVKA----SFAN 285
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 379 D--SNYPVMVLLGGCAALSTQCQLASYPLAVPTRMQAOAMLESPQUNMGJLFRRIIS 436
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 286 EDGQVSPPSLLL--AGALAGMPAASLVTPADVITKRRLVOYAAAGOTTYSVGVIDCERRKI LR 343
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 437 KEGIPGLYRGITPNEMKVLPAYGISVYVENKKQ 470
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 344 EEGPKALKWKAGARVERSSPOGCVTLITYELLQR 377
      | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-08-933-750C-19
; Sequence 19, Application us/08933750C
; Patent No. 5932442
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; APPLICANT: Au-Young, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Gugler, Karl J.
; APPLICANT: Corley, Neil C.
```

```

; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,750C
; FILING DATE: September 23, 1997
; CLASSIFICATION: 536
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNCOAT01
; CLONE: 724157
; US-08-933-750C-19

Query Match 10.3%; Score 255; DB 2: Length 351;
Best Local Similarity 23.1%; Pred. No. 1.3e-16;
Matches 79; Conservative 58; Mismatches 137; Indels 68; Gaps 9;

OY 196 ROLLAGGAGAVSRTSTAPLDRKIMQ----- 223
DB 13 QOMVASGTCGAVVTSLEMPRLDVVKVRLQSRPSMASSELMPSRLMSLSYTKKCLLYCNG 72
OY 224 -----VHGSK-----SDKWNIFG---GFRQWYKEGGISLMGNGTNNYIKIAPETAV 267
DB 73 VLEPLYLCPNGARCATWTFODPTFRGTMDAFVKIVRHGSTRMLSGLPATLVMTVPATAI 132
OY 268 KFWAVEQYKKLLTEBQKIGTFEERFISGSMAGATQTFIYPMVEVWKTRLAVGKTQOYSGI 327
DB 133 YFTATDQLKAFLCGRALTSDLTAPVAGALARLGTIVYISPLELMRTKLOAQHV-SYREL 191
OY 328 YDCAKKILKHESLGAIFYGYVGNLGIIPYAGIDLAIVYELLSKSYWLDNF-AKDSVNPQVM 386
DB 192 GACVTAATAVAGGWRSLMGWPTALRDVPFSALYWFNYELVKS-WLNLGRPRDQTSVCS 250
OY 387 VILGGALSTTCGOLASTPLALVTRRMOAQLBESSPOLNMVG-----LFRRIISKEGI 440
DB 251 FV--AGGISGTVAAVLTLPFDVVKTORQVALGMEAVVRNPLHVDSTWLLRRIRAESGT 308
OY 441 PELYRGITPNEFMKVLPAVGISVYVE-----NMKOTLG 473
DB 309 KGLFAGFLPRIKAAPSCAIMISTYEFKGSFFORLNDRLLG 350

RESULT 11
US-09-234-613-19
; Sequence 19, Application US/09234613
```

```

; Patent No. 6132973
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; APPLICANT: Au-Yang, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,613
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/933,750
; FILING DATE: September 23, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNCOAT01
; CLONE: 724157
; US-09-234-613-19

Query Match 10.3%; Score 255; DB 4: Length 351;
Best Local Similarity 23.1%; Pred. No. 1.3e-16;
Matches 79; Conservative 58; Mismatches 137; Indels 68; Gaps 9;

OY 196 ROLLAGGAGAVSRTSTAPLDRKIMQ----- 223
DB 13 QOMVASGTCGAVVTSLEMPRLDVVKVRLQSRPSMASSELMPSRLMSLSYTKKCLLYCNG 72
OY 224 -----VHGSK-----SDKWNIFG---GFRQWYKEGGISLMGNGTNNYIKIAPETAV 267
DB 73 VLEPLYLCPNGARCATWTFODPTFRGTMDAFVKIVRHGSTRMLSGLPATLVMTVPATAI 132
OY 268 KFWAVEQYKKLLTEBQKIGTFEERFISGSMAGATQTFIYPMVEVWKTRLAVGKTQOYSGI 327
DB 133 YFTATDQLKAFLCGRALTSDLTAPVAGALARLGTIVYISPLELMRTKLOAQHV-SYREL 191
OY 328 YDCAKKILKHESLGAIFYGYVGNLGIIPYAGIDLAIVYELLSKSYWLDNF-AKDSVNPQVM 386
DB 192 GACVTAATAVAGGWRSLMGWPTALRDVPFSALYWFNYELVKS-WLNLGRPRDQTSVCS 250
OY 387 VILGGALSTTCGOLASTPLALVTRRMOAQLBESSPOLNMVG-----LFRRIISKEGI 440
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Db 251 FV--AGISCTVAATLTPEDVYKTOQOVALGAMEAVRVNPDLHVDSTWLLRIRAESGT 308
QY 441 PGLYRGITPNEKMLPAVGISYVYE-----NMKOTLG 473
Db 309 KGLFAGFLPRLIKRAAPSCAIMISTYFEGKSFORLNDRLIG 350

RESULT 12
US-08-775-009-32
; Sequence 32, Application US/08775009
; Patent No. 5935783
; GENERAL INFORMATION:
; APPLICANT: Gong, Weijong
; APPLICANT: Emanuel, Beverly S.
; APPLICANT: Budarf, Marcia L.
; APPLICANT: Roe, Bruce
; TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digestion and
; TITLE OF INVENTION: Veliocardiofacial Syndrome Minimal Critical Region
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Mashburn Kurtz Mackiewicz &
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/775,009
; FILING DATE: 27-Dec-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yalco
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CH-0681
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 311 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-775-009-32

Query Match 9.7%; Score 239.5; DB 2; Length 311;
Best Local Similarity 25.4%; Pred. No. 3.5e-15;
Matches 74; Conservative 58; Mismatches 142; Indels 17; Gaps 7;

QY 196 ROLLAGGAGVARSRTAPLDRKIMQV-HGSKSDKMNIFGG-FRQMEGGIRSRMRG 253
Db 27 KALLAGLGGAGTCTFFPEYVKTQLOLDERSHPRRGIGCVROTIVSHGLGLYRG 86
QY 254 NGTNVIRIAPETAVMFAYEQYKLLTEEGOKIGTFEERFISGSMAG-ATQTFIYPMEM 312
Db 87 LSLVLSGIPKAVRFGMEFELSNHMRDAGRIDSTRGGLGAGVAGVAVVVCPRMETV 146
QY 313 KTLAVAGKIG--QYSGIYDCAKILKHESLGAFYKGYVNPULGIIPYAGIDLAAYELK 369
Db 147 KYVFIHQISPNKRYGFEHGVREIYVEOGIKGTGGLTATVTKOGSNOAIRFFVMTSLR 206
QY 370 SYVLNDPFAKDSVNP--GVVVLGCGALSTCGQLASYPALVTRTMOAAMEGSPQLN 426
Db 207 NWRGNDPKNRPMPLITGV-----GAIAGASVFGNTPLDVIKTRMQG--LEAHKYNR 258

QY 427 MGLFRRISKEGIPGLYRGITPNEKMLPAVGISYVYENMKOTLGTVOK 477
Db 259 TWDGGLQILKKEGLKAFYKGFPRIGRYCDAIVAFIYDEYKLLKNVWK 309

RESULT 13
US-08-518-878B-56
; Sequence 56, Application US/08518878B
; Patent No. 5702902
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/518,878B
; FILING DATE: 23-Aug-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Cornuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/88864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 299 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; US-08-518-878B-56

Query Match 9.4%; Score 233.5; DB 1; Length 299;
Best Local Similarity 25.3%; Pred. No. 1.3e-14;
Matches 75; Conservative 50; Mismatches 138; Indels 33; Gaps 9;

QY 197 QLLAGGAGVARSRTAPLDRKIMQVHGSKSDK-----NIFGGRQWYKBEGI 247
Db 6 KFLGAGTAACIADITPPLDPAKVRLOIGESOGPRVATVSAQYRGWGTILITVIREGP 65
QY 248 RSLMRGNGTNTKIAPEAVFAYEQYKLLTEEGOKIGTFEERFISGSMAGATAQFTIY 307
Db 66 RSLVNLVAGIQRMSASVARTIGLYDSYKQFTYTGSEHASTGSLLGSTGALAVAAQ 125
QY 308 PMEVMAKTRL-AVGKTG--QYSGIYDCAKILKHESLGAFYKGYVNPUL--GIIPYAGID 361
Db 126 PTDVVKVRFOQAQAGAGRRYQSTVNAYKTILAREGFRGLKGTSPNVARNAIVNCA--E 183
QY 362 LAYVELLKSYWLD-NFKKDSVNPQVWVLGCGALSTCGQLASTPLALVTRTMOAAME 420
Db 184 LVTYDLIKDLKLNMTDLPCHFTSAFAG--FCTVYIASPVDVVKTRYNNSALGQ 239
QY 421 ----GSPQLMWVGLFRRISKEGIPGLYRGITPNEKMLPAVGISYVYENMKOTL 472
Db 240 YSSAGHCAITM-----LQKSGPRAFYKGFMPFRLGSGNNVVMFVTEYDLKRAL 288

RESULT 14

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 18, 2002, 08:23:51 ; Search time 43.26 Seconds
(without alignments)
1059.515 Million cell updates/sec

Title: US-09-777-921A-2
Perfect score: 2481
Sequence: 1 MLRWLRDLPALPTACODAEQ.....VGISVYVENKQTLGVTK 477

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2373	95.6	475	2	T50686 peroxisomal Ca-dep
2	1103	44.5	588	2	T22688 hypothetical prote
3	991.5	40.0	531	2	G89667 protein FIVE.2 [1
4	988.5	39.8	587	2	T21074 hypothetical prote
5	852	34.3	479	2	T49871 peroxisomal Ca-dep
6	521	21.0	352	2	T01729 mitochondrial solu
7	520	21.0	332	2	T47703 Ca-dependent solu
8	506	20.4	358	2	T45934 hypothetical prote
9	500.5	20.2	500	2	T39385 probable mitochon
10	480.5	19.4	330	2	S26596 Graves disease mit
11	475	19.1	348	2	D84798 probable mitochon
12	455.5	18.4	415	2	T48171 hypothetical prote
13	454.5	18.3	381	2	T51158 hypothetical prote
14	448	18.1	325	2	T04273 adenylyate transloc
15	446	18.0	392	2	T05350 mitochondrial solu
16	430.5	17.4	349	2	A40141 mitochondrial solu
17	429.5	17.3	294	2	T22145 hypothetical prote
18	428	17.3	326	2	B40141 mitochondrial solu
19	425.5	17.2	418	2	B96811 hypothetical prote
20	425.5	17.2	436	2	T01459 Btl protein precur
21	417.5	16.8	326	2	S57544 probable membrane
22	392	15.8	326	2	T37874 probable membrane
23	377.5	15.2	494	2	S57539 probable membrane
24	369	14.9	298	2	B43646 ADP,ATP carrier pr
25	368	14.8	298	1	S03894 ADP,ATP carrier pr
26	365	14.7	357	2	S46795 ADP,ATP carrier pr
27	356	14.3	301	2	S51132 ADP,ATP carrier pr
28	355.5	14.3	386	2	S21974 ADP,ATP carrier pr
29	355.5	14.3	387	2	S14876 ADP,ATP carrier pr

30	355	14.3	298	2	I60173 adenine nucleotide
31	354.5	14.3	387	2	S16568 ADP,ATP carrier pr
32	354	14.3	305	2	S68154 ADP,ATP carrier pr
33	353.5	14.2	309	2	A24849 ADP,ATP carrier pr
34	353	14.2	298	2	S37210 ADP,ATP carrier pr
35	352.5	14.2	366	2	S17917 ADP,ATP carrier pr
36	352	14.2	298	1	A44778 ADP,ATP carrier pr
37	352	14.2	339	2	A41677 ADP,ATP carrier pr
38	351.5	14.2	318	1	A31978 ADP,ATP carrier pr
39	351	14.1	298	1	A29132 ADP,ATP carrier pr
40	349.5	14.1	382	2	S33630 ADP,ATP carrier pr
41	349.5	14.1	386	2	T09709 ADP,ATP carrier pr
42	348	14.0	298	1	XWBO ADP,ATP carrier pr
43	347	14.0	298	2	S31814 ADP,ATP carrier pr
44	346	13.9	385	1	S29852 ADP,ATP carrier pr
45	345	13.9	313	1	XWNC ADP,ATP carrier pr

ALIGNMENTS

Query Match	95.6%	Score 2373	DB 2	Length 475
Best Local Similarity	95.2%	Pred. No. 4.8e-149		
Matches 454	Conservative 12	Mismatches 9	Indels 2	Gaps 1
QY	1	MLRWLRDLPALPTACODAEPTRETLFOALDRMGDVNDIGELGRNLTGPIGDAAE	60	
DB	1	MLRWLRDLPALPTACODAEPTRETLFOALDRMGDVNDIGELGRNLTGPIGDAAE	60	
QY	61	EKFTTGVDVNRKDLDEEFEMKYLKDHEKKMKLAFKSLDKNNDKIRASEIVOSLQTLGL	120	
DB	61	EKFTTGVDVNRKDLDEEFEMKYLKDHEKKMKLAFKSLDKNNDKIRASEIVOSLQTLGL	120	
QY	121	TISEQDAELILQSIDVDGVTVDWNEWDYFLFNPTVDIEIIRFMKHSIGIDIGSLTI	180	
DB	121	TISEQDAELILQSIDVDGVTVDWNEWDYFLFNPTVDIEIIRFMKHSIGIDIGSLTI	180	
QY	181	PDEFTDEKSSGGWQWOLLAGTAGAASRSTAPLDLKTMMQVHGSKSKMNTFGFQRQ	240	
DB	181	PDEFTDEKSSGGWQWOLLAGTAGAASRSTAPLDLKTMMQVHGSKSKMNTFGFQRQ	240	
QY	241	MVEEGGIRSLMRNGTGVNIKIAETAVKFWAYQDKLLEESQKIGTFRRFISGSNAGA	300	
DB	241	MVEEGGIRSLMRNGTGVNIKIAETAVKFWAYQDKLLEESQKIGTFRRFISGSNAGA	300	
QY	299	TAOTFTIYPMVEMKTRILAVGKTQYSGIYDCAKKILKHGEGAFYKGVPMULGIIPYAGI	360	
DB	299	TAOTFTIYPMVEMKTRILAVGKTQYSGIYDCAKKILKHGEGAFYKGVPMULGIIPYAGI	360	
QY	361	DLAVVELLSKSWLNDFAKDSVNPNGVWVLGGGALSSCGOLASYPALAVYTRMOAAMLE	420	
DB	361	DLAVVELLSKSWLNDFAKDSVNPNGVWVLGGGALSSCGOLASYPALAVYTRMOAAMLE	420	
QY	421	GSPOLMVGILFRRIISKEGIPGLYRGITTFPMKVLPAVGISYVYVENKQTLGVTK	477	
DB	421	GSPOLMVGILFRRIISKEGIPGLYRGITTFPMKVLPAVGISYVYVENKQTLGVTK	477	

Db 419 GAPOLNMVGLFRRIRISKEGLPGHYRIRITFENMKVLPVAVGISYVVEENMKQTLCVYTK 475

RESULT 2

T22688

hypothetical protein F55A11.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T22688

R:Kershaw, J.

submitted to the EMBL Data Library, May 1996

A:Reference number: Z19600

A:Accession: T22688

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-388 <WIL>

A:Cross-references: EMBL:Z72511; PIDN:CA96658.1; GSPDB:GN00023; CESP:F55A11.4

A:Experimental source: clone F55A11

C:Genetics:

A:Gene: CESP:F55A11.4

A:Map position: 5

A:Introns: 24/1; 77/2; 277/3; 434/3; 474/1; 511/3; 531/3

Query Match	44.5%	Score 1103;	DB 2;	Length 588;
Best Local Similarity	45.7%	Pred. No. 3.9e-65;		
Matches 210; Conservative	104;	Mismatches 142;	Indels 4;	Gaps 3;

OY	19	EOPRREYELFALORNGGVADIELOEGRNIGLPIPGOAAEKEIFTTGVNKGDKIDEF	78
Db	73	EKERQIRIYDRLDINDGTTIDIDITDLALKHEPHIPLAMPALAYIMSKSPDEGRVDF	132
OY	79	EFMKYLKDEHKMKLAFKSLDKNDNGKIEASEIYOSLQTLGTTISEQAEELLQSIDVDB	138
Db	133	SFSSEVLNENOEKLEAMEPADNRNDHGDYDVAMKKNYCKDGVPLDHHKAOHYNKMDTG	192
OY	139	TMTYDMNMRBYFLFENPYTDIEELIIRPKKSTGTDIGDLSLTIDELFEDEKKSGOMWRQL	198
Db	193	SASVDLKEEDEFPMALYBSSDLKTDYDWRNHLIIDIQESODIPEDFSQOQMORGIMWRHL	252
OY	199	LAGGIAGAVSRSTAPDLRLKIMAYGVGSKDKNMINGEGRFOMWKEGGISLIRGNGTWN	258
Db	253	VAGGAGAVSTCTGAPFPRIMVYLDQVAMSKTNRLRGVMSCLLHAEBGKISPMRNGINYN	312
OY	259	IKIAPETAVKRWAYEYQYKLLTEE--GOKTGFERTISGMAGATAOTFYIPMEVAKTRL	316
Db	313	IKIPEBSAIFKEMCYDOJLKTLOKKKGKEHEISTEERLCAGSAGASISOSTIYIPMEVAKTRL	372
OY	317	AVGKTGOYS--GIYDOCAKKILKHEELGAFYGVYVNLGIIIPYAGIDLAVYELLKSYWLDN	375
Db	373	ALRKTGQDLRGIITHFAHKMYTKBEIRICFPYKGYLDNLGIIIPYAGIDLAITYETLKRTYYVR	432
OY	376	FAKDSGVNVVYLLGCGALSSTGQSLASYPALVYRTMQAOAMLEGSPOLN--MYGLFRRI	434
Db	433	YETNSSBEGVALLACGSCSTGQSLSSYPALVYRTLOALSTIRYSPQDWTGQFXYI	492
OY	435	ISKBEIGBLYGITPNPMKULPANGISIVYVYENMKOTLGV	474
Db	493	LONEGVTFYRGITPNPLKLYPAVISIYVYVEKRTLGV	532

RESULT 3
G89667
protein F17E5.2 [imported] - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 10-May-2001 #sequence, revision 10-May-2001 #text, change 09-Nov-2001
C:Accession: G89667
R:anonymous, The C. elegans Sequencing Consortium.
S:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
S:Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
A:Reference number: A75000; MIMD:99066613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: G89667
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-531 <STO>
A:Cross-references: GB:chr_X; PIDN:CAA90761.1; PID:g3876012; GSPDB:GN00028; CESP:FL7E
C:Genetics:
A:Gene: FL7E5.2
A:Map position: X

Query Match	40.0%	Score 991.5;	DB 2;	Length 531;
Best Local Similarity	42.3%	Pred. No. 7.7e-58;		
Matches 203; Conservative	92;	Mismatches 138;	Indels 47;	Gaps 8;

```

0Y 16 ODAEPYVEYELLFALBRNNGVADIELOEGJFNILGIPGDAEKEEIKFTTGVNNDGKI 75
11 QNISLSTIRMYRBLDANDNGSIDIDRLQAL-SIQAHIPASVAPRLLEMRKSEHSDRY 69
0Y 76 DFEEMKYLKDHEKMKMLAEKSLDKNNDKIEASEIYOSIQTGLTISEQOAEILLQSID 135
Dd 70 TYADETNVIVAEHRLAEVEFKIDINLSDGEYDAEIKSYCKEMGVNLDQKAMSIRKMD 129
0Y 136 VDGJTVNMNBRXYELFNPYDIEELIRPKHSTG-----IDIGDSL 178
Dd 130 QSGSSVWLNEFOPMLYBPTSDRWDVDRHNLVCTCESNSRRFTQNFQIIDIEDG 189
0Y 179 TIPDETFDEKSGQWWRQOLLJAGIAGVASTRTAPLDRKLE-----M 221
Dd 180 QVPDEFJFQELLSGVWHRHLVAGSVAGMSPTCAPDRIKYVLLQWVYLLHLEHMEKLA 249
0Y 222 MOVHSGSKDKNNITNGGFROWKBECSISLMRGNTNYIKIAPETAYKFNAYEOKYKULLE 281
Dd 250 LQVNSTKNNKGVVSCVHLIABEGISFPMGNCINVIKIIAPESAMFKMYDIDKRMWDE 309
0Y 282 --EOKICTFERETISGMAGATQFTFYPEWVMKTRILAVKTCQY-SGIYDCAKKTILKE 338
Dd 310 YKGGAEIETIERLLAGSSAGAIISQTAIYPEWVKTRILAKRTQLQDKGMFHPAKMYTKE 369
0Y 339 GIGAFYKGVNPLGIIPYAGIDILAVYELKSYWLDNPFARDVNPQVWVLLSCGALSSTC 398
Dd 370 GIKCFYKCYLPLNLLGIIPYAGIDILVYESLKSMT--TRYTEHNEPGLALLACGTSSTC 428
0Y 399 GOLAFYPLAVTRFROQOAMLEGGPOLN-----WYGLFRRLISEGJIPGLYRBITNENK 453
Dd 429 GOLAFYPLAVTRFROQAAAI---SPKNSSTOPDWGQFKHILQEGFTGLYRBITNENK 485

```

```

RESULT 4
T21074
hypothetical protein F17E5.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T21074
R:McMurray, A.
submitted to the EMBL Data Library, August 1995
A:Reference number: Z19368
A:Accession: T21074
A>Status: preliminary; translated from GB/EMBL/DDBT
A:Molecule type: DNA
A:Residues: 1-587 <MWL>
A:Cross-references: PDB:Z50873; PIDN:CAA90761.2; GSPDB:GN00028; CESP:F17E5.2
C:Experimental source: clone F17E5
C:Genetics:
A:Gene: CESP:F17E5.2
A:Map position: X
A:Introns: 21/1; 48/3; 74/2; 111/3; 183/2; 384/1; 432/3; 503/1; 541/3

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Query	19	EQPTRETFQALDRRGDSVDIGELQELRLNLGPIGDAAEKEFTTSDVKKDKLPFE	78
Query Match	39.88;	Score 988.5;	DB 2; Length 587;
Best Local Similarity	42.3%;	Pred. No. 1.4e-57;	
Matches	202;	Conservative	91; Mismatches 137; Indels 47; Gaps 8;

Db 327 DPQDVKLPGNLVMAFGALSGSTGATVFPPLNLTIRLQTOGSHAPATYDG-----FIDC 381
 QY 431 FRRISKEGIPGLYRGITPFPKVLPAVGISVYVENMKOTGV 474
 Db 382 FFKTTKNEGFRGLYKGLSPNLKLVADVAISIVLYENCKKMWGL 425

RESULT 10

526596

Graves disease mitochondrial solute carrier protein - bovine

C.Species: Bos primigenius taurus (cattle)

C.Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999

C.Accession: S26596; 146022

R.Flemonete, G.; Runswick, M.J.; Walker, J.E.; Palmeri, F.

submitted to the EMBL Data Library, May 1992

A.Description: Sequence and pattern of expression of a bovine homologue of a human mitoc

A.Reference number: S26596

A.Accession: S26596

A.Status: preliminary

A.Molecule type: mRNA

A.Residues: 1-330 <FID>

A.Cross-references: EMBL:X66035; NID:g386; PIDN:CAA6834.1; PID:g387

R.Flemonete, G.; Runswick, M.J.; Walker, J.E.; Palmeri, F.

DNA Seq. 3, 71-78, 1992

A.Title: Sequence and pattern of expression of a bovine homologue of a human mitochontri

A.Reference number: 146022; MUID:93091248

A.Accession: 146022

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-330 <FID>

A.Cross-references: EMBL:X66035; NID:g386; PIDN:CAA6834.1; PID:g387

C.Genetics:

A.Gene: GDC

C.Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C.Keywords: cardiac muscle; duplication; heart; mitochondrion; transmembrane protein

E/125-119/Domain: ADP, ATP carrier protein repeat homology <ACPI>

F/125-215/Domain: ADP, ATP carrier protein repeat homology <ACPI>

F/235-327/Domain: ADP, ATP carrier protein repeat homology <ACPI>

Query Match 19.4%; Score 480.5; DB 2; Length 330;
 Best Local Similarity 38.1%; Pred. No. 2.1e-24;
 Matches 112; Conservative 54; Mismatches 109; Indels 19; Gaps 8;

QY 194 WROLLAGTAVGAVSRSTAPLDRLKIMQVHSGSKDNKINGFGFQMKREGIRSLMRG 253
 Db 34 WLRSLAGTACCAKTTIAPLDKRVKVLQAHNHHYRHLGVSTLPAVKKBEYGLYRG 93
 QY 254 NCTNVKIAPIETAVKFAVEYOYKLLTERGOKIGTFEPISSGAGATQTFIYPMEMVK 313
 Db 94 NCAMMIRIPYGAIDQFMAEHKTLITTKLGVSCHVHRLMAGSMGMTAVICTYPLDMVR 153
 QY 314 TRLAVKGTQ--YSGTYDCAKILKHEG--LCAFTKGYVPLNLTGTPVAGIDLAVELLK 369
 Db 154 VRLAFOVKGHEHYTGTIHAFTIYAKEGGFLG--FYRGLMPTILGMAPYAGVSFFETGLK 212
 QY 370 SYWLNEFA-----KDSVYGVNVL-----LGGALSSFCGGLASPLAVLRMAQAM 418
 Db 213 SYGL--SYAPTLGLGRSSDNPNVNLKTHNLGCGVAGAIADTISTPDPVTRRRMOLGV 271
 QY 419 L-EGSPOLNMGVLFRRISKEGI-DGLYRGITPFPKVLPAVGISVYVENMKO 470
 Db 272 LPEFKCLMRTMKYVYGHGIRGLYGLSLNTRYRCVPQSAVATYTELKMO 325

RESULT 11

DB4798

Probable mitochondrial carrier protein [imported] - Arabidopsis thaliana

C.Species: Arabidopsis thaliana (mouse-ear cress)

C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C.Accession: DB4798

R.Li, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umeyam, L.; Tallon, L.

uess, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402, 761-768, 1999

A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A.Reference number: A84420; MUID:20083487

A.Accession: DB4798

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-348 <STO>

A.Cross-references: GB:AE002093; NID:g4895195; PIDN:AAD32782.1; GSPDB:GN00139

C.Genetics:

A.Gene: Atg37890

A.Map position: 2

C.Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C.Keywords: mitochondrion

Query Match 19.1%; Score 475; DB 2; Length 348;
 Best Local Similarity 36.7%; Pred. No. 5.2e-24;
 Matches 114; Conservative 52; Mismatches 103; Indels 42; Gaps 9;

QY 195 WROLLAGTAVGAVSRSTAPLDRLKIMQVHSGSKD-----KNITGFGFQMKREGIRSLMRG 249
 Db 42 FQNLGAGTAVGAVSRSTAPLDRLKIMQVHSGSKD-----KNITGFGFQMKREGIRSLMRG 101
 QY 250 LMRGNGTNVKIAPIETAVKFAVEYOYKLLTER-----GOKIGT--FEPISSGAGAT 301
 Db 102 FMKGNLVTVYHRIPTAVNFAVEYKTLFNSNPVQSFIGNTSGNPVYFVSGGLAGIT 161
 QY 302 AQTFIYPMEMVKTRFLAVGKTG--OYSGTYDCAKILKHEGIAFYKGVNPLNLTGTPVAGI 360
 Db 162 AATATVPLDLVTRRLAQRNAIYVGGIEHFTFRTCREGILGYKGLAVLLGVPGLAI 221
 QY 361 DLAVYFELKSYWLDNFAKDS-----VNRGVNVLGGALSSFCGGL-----ASTPLA 407
 Db 222 NEFAVYSMKLEFWSHHPNDSDLVLSVSGL-----AGAVSYDDDKLFDAHNVAVATPLD 276
 QY 408 LVYTRMAQAMLEGSP-----OLNMVGLFRRISKEGIPGLYRGITPFPKVLPAVGIS 461
 Db 277 LVYRRMQ-----VAGAGRAVYNTGLGFTKHLFKSGFGITRGILPEYKVVPGVGI 332
 QY 462 YVYVENMKOTL 472
 Db 333 FMTYDALRLL 343

RESULT 12
 T48171
 hypothetical protein F7A7.20 - Arabidopsis thaliana
 C.Species: Arabidopsis thaliana (mouse-ear cress)
 C.Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C.Accession: T48171
 R.Beaven, M.; Terryn, N.; Ardiles, W.; Buyschaert, C.; Dasseville, R.; De Clerck, R.;
 ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, March 2000
 A.Reference number: Z24487
 A.Accession: T48171
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-415 <BEV>
 A.Cross-references: EMBL:AL161946
 A.Experimental source: cultivar Columbia; BAC clone F7A7
 C.Genetics:
 A.Map position: 5
 A.Introns: 144/3; 163/3; 184/3; 203/3; 231/3; 254/3; 292/2; 349/1; 375/2
 A.Note: F7A7.20

Query Match 18.4%; Score 455.5; DB 2; Length 415;
 Best Local Similarity 33.1%; Pred. No. 1.3e-22;
 Matches 107; Conservative 66; Mismatches 115; Indels 35; Gaps 8;
 QY 177 SLTIPEFTDEKKSQWNR-----LLAGGAGAVSRSTAPLDRLKIM 222
 Db 177 SLTIPEFTDEKKSQWNR-----LLAGGAGAVSRSTAPLDRLKIM 222

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 09:23:05 ; Search time 24.8 Seconds
(without alignments)
744.727 Million cell updates/sec

Title: US-09-777-921A-2
Perfect score: 2481
Sequence: 1 MLRWLRDFALEPTACODAEQ.....VGISVYVENMKQTIGVTQK 477

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:.*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1103	44.5	588	1	CMC2_CAEEL
2	988.5	39.8	587	1	CMC3_CAEEL
3	611.5	24.6	545	1	CMC1_YEAST
4	480.5	19.4	330	1	GDC_BOVIN
5	454.5	18.3	332	1	GDC_HUMAN
6	428	17.3	322	1	GDC_RAT
7	425.5	17.2	436	1	BTL1_MAIZE
8	392	15.8	326	1	YE08_SCHPO
9	369	14.9	298	1	ADT3_BOVIN
10	368	14.8	298	1	ADT3_HUMAN
11	365	14.7	357	1	LEU5_YEAST
12	360	14.5	298	1	ADT2_MOUSE
13	359	14.5	298	1	ADT2_HUMAN
14	358	14.4	298	1	ADT2_RAT
15	355.5	14.3	386	1	ADT1_SOLTU
16	355.5	14.3	387	1	ADT1_MAIZE
17	355	14.3	298	1	ADT1_MOUSE
18	355	14.3	298	1	ADT1_RAT
19	354.5	14.3	387	1	ADT2_MAIZE
20	354	14.3	305	1	ADT1_KULULA
21	353.5	14.2	309	1	ADT1_YEAST
22	352	14.2	298	1	ADT1_HUMAN
23	352	14.2	339	1	ADT1_CHLKE
24	351.5	14.2	318	1	ADT2_YEAST
25	350.5	14.1	382	1	ADT2_ORYSA
26	349.5	14.1	386	1	ADT1_GOSHI
27	348	14.0	297	1	ADT1_BOVIN
28	346.5	14.0	331	1	ADT1_WHEAT
29	346	13.9	385	1	ADT2_ARATH
30	345	13.9	313	1	ADT1_NEUCR
31	344	13.9	381	1	ADT1_ARATH
32	341.5	13.8	331	1	ADT2_WHEAT
33	340	13.7	322	1	ADT1_SCHPO

34	339.5	13.7	307	1	ADT3_YEAST	P18238 saccharomyc
35	337	13.6	301	1	ADT1_ANOGA	O27238 anopheles g
36	337	13.6	386	1	ADT2_SOLTU	P27081 solanum tub
37	330.5	13.3	297	1	ADT1_DROME	O26365 drosophila
38	326.5	13.2	308	1	ADT1_CHLKE	P27080 chlamydomon
39	322.5	13.0	322	1	SFC1_YEAST	P33303 saccharomyc
40	318	12.8	314	1	YG20_YEAST	P53257 saccharomyc
41	314.5	12.7	315	1	MFT_HUMAN	O9h281 homo sapien
42	311	12.5	695	1	CMC1_DROME	O9va73 drosophila
43	303.5	12.2	373	1	Y1A6_YEAST	P40536 saccharomyc
44	295.5	11.9	702	1	CMC1_CAEEL	O21153 caenorhabdi
45	295	11.9	320	1	DNC_HUMAN	O9h221 homo sapien

ALIGNMENTS

RESULT	ID	CMC2_CAEEL	STANDARD:	PRT:	588 AA.
AC	020759:				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DE	Probable calcium-binding mitochondrial carrier F55A11.4.				
GN	F55A11.4.				
OS	Caenorhabditis elegans.				
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;				
OC	Rhabditidae; Peloderinae; Caenorhabditis.				
OX	NCBI_Taxid=6239;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-BRISTOL NZ;				
RA	Kershaw J.;				
RL	Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: CALCIUM-DEPENDENT MITOCHONDRIAL SOLUTE CARRIER (BY				
CC	SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL				
CC	INNER MEMBRANE (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. ARALAR				
CC	SUBFAMILY.				
CC	-1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
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CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
DR	EMBL: Z72511; CAA9658.1. -				
DR	WormPep: F55A11.4; CE05946.				
DR	InterPro: IPR002048; EF-hand.				
DR	InterPro: IPR002067; Mt_carrier.				
DR	InterPro: IPR001993; Mitoch_carrier.				
DR	Pfam: PF00036; efhand; 3				
DR	Pfam: PF00153; mito_carr; 3.				
DR	PRINTS: PR00926; MITOCARRIER.				
DR	SMART: SM00054; Efh; 3.				
DR	PROSITE: PS00018; EF_HAND; 2.				
DR	PROSITE: PS00215; MITOCH_CARRIER; FALSE NEG.				
KW	Hypothetical protein: Mitochondrion: Inner membrane: Repeat;				
KW	Transmembrane; Transport; Calcium-binding.				
FT	TRANSMEM 252				
FT	TRANSMEM 307				
FT	TRANSMEM 352				
FT	TRANSMEM 403				
FT	TRANSMEM 446				
FT	TRANSMEM 504				
FT	CA_BIND 52				
FT	CA_BIND 86				
FT	DOMAIN 123				
FT	ANCESTRAL CALCIUM SITE 3.				

FT CA_BIND 153 164 EF-HAND 4.
FT DOMAIN 189 535 3 APPROXIMATE TANDEM REPEATS.
FT REPEAT 189 335 1.
FT REPEAT 336 429 2.
FT REPEAT 430 535 3.
SQ SEQUENCE 588 AA: 66336 MW: 68DDF60923D8697D CRC64:

Query Match 44.5%; Score 1103; DB 1; Length 588;
Best Local Similarity 45.7%; Pred. No. 1.9e-64;
Matches 210; Conservative 104; Mismatches 142; Indels 4; Gaps 3;

QY 19 EDPTRYETLFOALDRNGDGVNDIGELQEGRLNLGIPLGDADEKFTTGGVNDKDKLDFE 78
D 19 EDPTRYETLFOALDRNGDGVNDIGELQEGRLNLGIPLGDADEKFTTGGVNDKDKLDFE 78
D 73 EKERQIRDIYDLIDNNGTIDIRDLTLAKHETPHIPANLAPVIMSKSPDDEGRVDFY 132
QY 79 EFMKYLKHEKKMKLAFKSLDKNNDKGKIEASIVOSLQTLGITIEQOALLQSIDVNG 138
D 79 EFMKYLKHEKKMKLAFKSLDKNNDKGKIEASIVOSLQTLGITIEQOALLQSIDVNG 138
D 133 SFSSVYLENEQKLAEMFADMDRNDHGLDVVEMKNYCKDIGVPLDHRKQHTVKNMDQYG 192
QY 139 TMTVDMNEMRDYFLPNPYTDIEEIRFMKHSYDIDGSLTIPDEFTEDEKSGOMWROL 198
D 139 TMTVDMNEMRDYFLPNPYTDIEEIRFMKHSYDIDGSLTIPDEFTEDEKSGOMWROL 198
D 193 SASVDLKEFQEFMMLYPSDDLKDIDYDFWRHNLIDIGESQIPDEFSQOEMQEGIMWRHL 252
QY 199 LAGGIAVARTSTAPLDRLKTMQVHSGSDKNIFFGSRQMKVKGIRSLMRNGTIV 258
D 199 LAGGIAVARTSTAPLDRLKTMQVHSGSDKNIFFGSRQMKVKGIRSLMRNGTIV 258
D 253 VAGGAAGAVSRCTAPFRIRKIVYLQVNSKTNLGVMSCLKHLAEGKISFRMNGINAV 312
QY 259 IKIAETAVKPMAYEYOKYKLLTEE--GOKIGFEERFISGSMGATAPFIYMEYKPTL 316
D 259 IKIAETAVKPMAYEYOKYKLLTEE--GOKIGFEERFISGSMGATAPFIYMEYKPTL 316
D 313 IKIAESAKIKFQCYDLKRLQKKGNEISTFERLCSASAGALSQSTIYMEYKPTL 372
QY 317 AVGKTGYTS-GIYDCAKILKHEGLAFYKGYVPMNLGIIPYAGIDLAVYELLSKSYWLDN 375
D 317 AVGKTGYTS-GIYDCAKILKHEGLAFYKGYVPMNLGIIPYAGIDLAVYELLSKSYWLDN 375
D 373 ALRKTGQDRGIIHFAHKMYTEGIRCFYKGYLPNLIGIIPYAGIDLAVYELLSKSYWLDN 432
QY 376 FAKDSVNVGVNVLCCGALSTCGOLASTPLAVTRMOAQMLESQPOLN-MVGLFRRI 434
D 376 FAKDSVNVGVNVLCCGALSTCGOLASTPLAVTRMOAQMLESQPOLN-MVGLFRRI 434
D 433 YETNSSEPRVLALACGTCSSQSYSPALVTRLOALSITRYSPOPTMFGQFKYI 492
QY 435 ISKEGIPGLYRGITPNPMKLVPAVGSIVYVENMKOTLGV 474
D 435 ISKEGIPGLYRGITPNPMKLVPAVGSIVYVENMKOTLGV 474
D 493 LONEGVATGYRGITPNPMKLVPAVGSIVYVENMKOTLGV 532

RESULT 2
CMC3_CABEL STANDARD: PRT: 587 AA.
AC Q19529;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable calcium-binding mitochondrial carrier F17E5.2.
GN F17E5.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CALCIUM-DEPENDENT MITOCHONDRIAL SOLUTE CARRIER (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. ARALAR
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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DR EMBL: Z50873; CA90761.2; -.
DR WormPep: F17E5.2; CE23667.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR002067; Mit-carrier.
DR InterPro: IPR001993; Mitoch-carrier.
DR Pfam: PF00036; ethand; 3.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR SMART: SM00054; EFh; 2.
DR PROSITE: PS00018; EF_HAND; 2.
DR PROSITE: PS00215; MITOCH_CARRIER; FALSE NEG.
KM Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
KW Transmembrane; Transport; Calcium-binding.
FT TRANSMEM 265 282 1 (POTENTIAL).
FT TRANSMEM 337 356 2 (POTENTIAL).
FT TRANSMEM 382 395 3 (POTENTIAL).
FT TRANSMEM 433 452 4 (POTENTIAL).
FT TRANSMEM 475 492 5 (POTENTIAL).
FT TRANSMEM 534 551 6 (POTENTIAL).
FT CA_BIND 49 60 EF-HAND 1.
FT CA_BIND 83 94 EF-HAND 2.
FT DOMAIN 119 129 ANCESTRAL CALCIUM SITE 3.
FT CA_BIND 149 160 EF-HAND 4.
FT DOMAIN 185 563 3 APPROXIMATE TANDEM REPEATS.
FT REPEAT 185 365 1.
FT REPEAT 366 459 2.
FT REPEAT 460 563 3.
SQ SEQUENCE 587 AA: 65906 MW: 19E62936D5A17021 CRC64:

Query Match 39.8%; Score 988.5; DB 1; Length 587;
Best Local Similarity 42.3%; Pred. No. 5e-57;
Matches 202; Conservative 91; Mismatches 137; Indels 47; Gaps 8;

QY 19 EDPTRYETLFOALDRNGDGVNDIGELQEGRLNLGIPLGDADEKFTTGGVNDKDKLDFE 78
D 19 EDPTRYETLFOALDRNGDGVNDIGELQEGRLNLGIPLGDADEKFTTGGVNDKDKLDFE 78
D 70 EKKKIRDMYDLDLDNDGSDIDRLTQAL-SLOAHIPASVAPKLLERKSHSDRYTA 128
QY 79 EFMKYLKHEKKMKLAFKSLDKNNDKGKIEASIVOSLQTLGITIEQOALLQSIDVNG 138
D 79 EFMKYLKHEKKMKLAFKSLDKNNDKGKIEASIVOSLQTLGITIEQOALLQSIDVNG 138
D 129 DFTNVVIAHEARLAVPEKIDILNSDGEVMAETKSYCKEMGVNLDQKMSIVKMDQSG 188
QY 139 TMTVDMNEMRDYFLPNPYTDIEEIRFMKHSYDIDGSLTIP 181
D 139 TMTVDMNEMRDYFLPNPYTDIEEIRFMKHSYDIDGSLTIP 181
D 189 SSSVNLNEFQDMLLYPSTDMRMDVDFWRHNLVCTCLESNSRFRTOQIDIGDGOVP 248
QY 182 DEFTDEKSGQWMBOLLAGTAGAVSRSTAPLDRLKI-----MMQV 224
D 182 DEFTDEKSGQWMBOLLAGTAGAVSRSTAPLDRLKI-----MMQV 224
D 249 EDFTQELLISGVMMRHLVAGAVAGASRCTAPFRIRKIVYLQVNLGILFHTMFLKALQV 308
QY 225 HGSKSDKNIFGSGFROMYKGGIRSLMRNGTIVIKIAETAVKPMAYEYKLLTEE--E 282
D 225 HGSKSDKNIFGSGFROMYKGGIRSLMRNGTIVIKIAETAVKPMAYEYKLLTEE--E 282
D 309 NSTKTNKLGAVSCVHLNHEGKISFRMNGINIVIKIAESAMKFMICYDQIKRMWQEVKG 368
QY 283 GOKIGTFEERFISGSMGATAPFIYMEYKPTLAVKGTGY--SGIYDCAKILKHEGLG 341
D 283 GOKIGTFEERFISGSMGATAPFIYMEYKPTLAVKGTGY--SGIYDCAKILKHEGLG 341
D 369 GAEISTIEELLASGALISQTAIYPMYKTRLARTRGQDKGMFHFANHKMYTKEGIR 428
QY 342 AFYKGVNPLGIIYAGIDLAVYELLSKSYWLDNPAKOSVNGVWLLCGALSTCGOL 401
D 342 AFYKGVNPLGIIYAGIDLAVYELLSKSYWLDNPAKOSVNGVWLLCGALSTCGOL 401
D 429 CFYKGLPMLSLIIPYAGIDLAVYELLSKSYW--TKYTTETEGVALLACGTCSSCGOL 487
QY 402 ASYPLAVTRMOAQMLESQPOLN-----MVGLFRRIISKEGIPGLYRGITPNPMK 453
D 402 ASYPLAVTRMOAQMLESQPOLN-----MVGLFRRIISKEGIPGLYRGITPNPMK 453
D 488 ASYPLAVTRMOAQMLESQPOLN-----SPKNSGTQPTWVGQGRKHLQDGLGFLYRGITPNPMK 541


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RESULT 3
ID CMCL_YEAST STANDARD: PRT: 545 AA.
AC P48233:
DT 01-FEB-1996 (rel. 33, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Probable calcium-binding mitochondrial carrier YNL083W.
GN YNL083W OR N2312.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=96310628; PubMed=8740422;
RA Soler-Mira A., Salz J.E., Ballesta J.P.G., Remacha M.;
RT "The sequence of a 17,933 bp segment of Saccharomyces cerevisiae
RT chromosome XIV contains the RHO2, TOP2, MKT1 and END3 genes and five
RT new open reading frames.";
RL Yeast 12:485-491(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE=96267764; PubMed=8701611;
RA Poehlmann R., Philippsen P.;
RT "Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV
RT reveals 12 new open reading frames (ORFs) and an ancient duplication
RT of six ORFs.";
RL Yeast 12:391-402(1996).
RN [3]
RP REVISIONS TO C-TERMINUS.
RX MEDLINE=97321806; PubMed=9178508;
RA el Moualij B., Duyckaerts C., Lamotte-Brasseur J., Sluse F.E.;
RT "Phylogenetic classification of the mitochondrial carrier family of
RT Saccharomyces cerevisiae.";
RL Yeast 13:573-581(1997).
CC -1 FUNCTION: CALCIUM-DEPENDENT MITOCHONDRIAL SOLUTE CARRIER (BY
CC SIMILARITY).
CC -1 SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (potential).
CC -1 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY. ARALAR
CC SUBFAMILY.
CC -1 SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -1 CAUTION: REF.1 AND REF.2 SEQUENCES DIFFER FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 403.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X89016; CA61427.1; ALT_FRAME.
DR EMBL: 271359; CA95958.1; ALT_FRAME.
DR SGD: S0005027; YNL083W.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR002067; Mt_carrier.
DR Pfam: PF00036; ehand; 3.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00018; EF_HAND; 1.
DR PROSITE: PS00215; MITOCH_CARRIER; 1.
KM Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
KV Transmembrane; Transport; Calcium-binding.
FT TRANSMEM 231 248 1 (POTENTIAL).
FT TRANSMEM 307 326 2 (POTENTIAL).
FT TRANSMEM 355 368 3 (POTENTIAL).
FT TRANSMEM 409 428 4 (POTENTIAL).

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FT TRANSMEM 458 475 5 (POTENTIAL).
FT TRANSMEM 516 535 6 (POTENTIAL).
FT CA_BIND 59 70 EF-HAND 1.
FT CA_BIND 93 104 EF-HAND 2.
FT DOMAIN 127 136 ANCESTRAL CALCIUM SITE 3.
FT CA_BIND 155 166 EF-HAND 4.
FT DOMAIN 191 191 1.
FT REPEAT 191 335 3 APPROXIMATE TANDEM REPEATS.
FT REPEAT 336 435 2.
FT REPEAT 436 545 3.
SQ SEQUENCE 545 AA; 61224 MW; B0CC2309AE759AA9 CRC64;

Query Match 24.6%; Score 611.5; DB 1; Length 545;
Best Local Similarity 28.3%; Pred. No. 1.3e-32;
Matches 155; Conservative 107; Mismatches 190; Indels 95; Gaps 15;

OY 15 CQ-DADQPTREYETLFDALDRNGDGVVDIGELQGLRMIGLPL--GQDAEKKIFFTGDYVK 71
DB 6 CETDKQDRIDRYACLPFKELDYKNGQVTLDMNLISAFENKDHPLGNDPAIKMLFTAMDYVK 65
OY 72 DGLDFEPEPKYIKLDEKKMKLAFKSLDKNNDKIEASEI---VQSLQTLGLTISEQAE 128
DB 66 DSVVDLSDFKKYASNAESQIWMNGFORDIDHDGKIGINEIRYLSLDLDNQSICNNELNHE 125
OY 129 LIIQSID-----VDCMTVDMNEMRDYF 151
DB 126 LSNKKVKKSRFPFEMAPPKRKANIALRGQASHKKNNDNRSKTTSDDLYVYDQWDFL 185
OY 152 LFNPTVDIEI---IRFNKSTGIDI---GDSLTIPDEFTEDEKSGQMMROLLAGIA 204
DB 186 LLYPRKQGSRLHTAYSYFLFNEDVDLSSEG--VTLLNDI-----RQGFPIAGIS 237
OY 205 GAVSRSTAPLDPLKIMQVH-----GSKSDKM-----NIFGFRQMK 243
DB 238 GVISRCTAFPDRLKFLIARTDLSLILNSKTDLLAKNPADINKISSPLAAVKLYR 297
OY 244 EGGIRSLMRNGNINVIKIAETFAFMAYEQYKILTE-BG-----QKIGFERISGS 298
DB 298 QGGIRKAFYVGNLNVKIPPESSIKFGSEFYTKIMKLKSGCRDTPKLSFSTIYAGLA 357
OY 299 GATAGTFIYPMEMKTRLAGV---KTGQSGIYDCAKKILKEGLGAFKGYVPLNGI 354
DB 358 GMAQGSVYVIDTLKFRVQCAPLDTKLKGNLLFQFAKDMFREGVALFRGVYVIGI 417
OY 355 ITPAGIDLAVYELKSTWLD-----NEAKDSVNPQVMVLLGCAIASSTGQGLASYPAL 408
DB 418 FPYAALDLGTFSAIKKWKYIAKQAKTLNLPQDOVTLNLVLPMAFGFAGSVYVPI 477
OY 409 VTRFMQAQMLESPQLN--VGLFRRIISKEGIPGLYRGITPDMKYLPAVGSIVYVEN 467
DB 478 LKRLDAQGYAHHPYVYNGFKVDLKLTLREGYQGLKGLVPLAKVPAVSISYLCYEN 537
OY 468 MKQPLGV 474
DB 538 LKKFMNL 544

RESULT 4
ID GDC_BOVIN STANDARD: PRT: 330 AA.
AC Q01888:
DT 01-APR-1993 (rel. 25, Created)
DT 01-APR-1993 (rel. 25, Last sequence update)
DT 01-MAR-2002 (rel. 41, Last annotation update)
DE Grave's disease carrier protein (GDC) (Mitochondrial solute carrier
DE protein homolog).
GN SLC25A16 OR GDA OR GDC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart:
RX MEDLINE=93091248; PubMed=1457817:
RA Flernmonte G., Runswick M.J., Walker J.E., Palmieri F.:
RT "Sequence and pattern of expression of a bovine homologue of a human
RL mitochondrial transport protein associated with Grave's disease.";
DNA Seq. 3:71-78(1992).
CC -1- FUNCTION: Required for the accumulation of coenzyme A in the
CC mitochondrial matrix (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane (By similarity).
CC -1- TISSUE SPECIFICITY: MOSTLY IN THYROID, LIVER, LUNG, KIDNEY AND
CC TO A LESSER EXTENT IN HEART AND SKELETAL MUSCLE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC CC
CC DR EMBL; X66035; CA446834.1; -.
CC DR PIR; S26596; S26596.
CC DR InterPro; IPR002067; Mit_carrier.
CC DR InterPro; IPR001993; Mitoch_carrier.
CC DR Pfam; PF00153; mito_carr; 3-
CC DR PRINTS; PR00926; MITOCARRIER.
CC DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT FT TRANSMEM 132 152 POTENTIAL.
FT FT TRANSMEM 189 209 POTENTIAL.
FT FT TRANSMEM 232 252 POTENTIAL.
FT REPEAT 1 121 1.
FT REPEAT 122 217 2.
FT REPEAT 218 330 3.
SQ SEQUENCE 330 AA; 36085 MM; 4C614701D2B8DEA9 CRC64;

Query Match 19.4%; Score 480.5; DB 1; Length 330;
Best Local Similarity 38.1%; Pred. No. 2.3e-24;
Matches 112; Conservative 54; Mismatches 109; Indels 19; Gaps 8;

QY 194 WROLLAGIAGAVSTRSTARPLRLIKIMQVHGSKDKNIFGGRQWYKEGSIKSLMWG 253
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
Db 34 WLRSFLAIGVCCAKCTVAPRLDRVKVLTQLAHNNHYRLHGVSFTLRAPVKKEGYLGKVG 93
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
QY 254 NGTVNIKRIAPETAVKFMAYEDQYKILLTEEGCKIGIFERFISSMAGATPOTIYMEYVK 313
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
Db 94 NGAMKIRLEPFGALQFMAFENHKYLLITTKLGVSGVHNRLMASMSGMTAPVICTYPLDMVR 153
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
QY 314 TRLAVALGKQ--YSGYISCAKKILKHEG--LGAFFKGVVNNLGIITPYAGIDLAVYELIK 369
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
Db 154 VRLAFQVNGEHTYGLIINAFPTIYAKKEGFLG-FRGLMPTILGNAPAGVSEFFFGFLIK 212
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
QY 370 SYWLNDFA-----KDSVNGVYVL-----LCCGALSTCGOLASTPLALVTRQAOAM 418
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
Db 213 SVGLT-SVAPTLGLRPSSDNPVLYLKTGINLLCGGVAAIMQTIYSIPDVTFRRQLAV 271
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
QY 419 L-EGSPQIANNVGLFRIRISKEGI--GLRGTGTPNPMKVLPAVGISVYVYENKKQ 470
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I
Db 272 LPEFKCLTMEETMKYUYGHNQIRKGLIRGLISLNIIRCVPSQAVAFITYELMKQ 325
   I I I I I I I I I I I I I I I I I I I I I I I I I I I I I I

RESULT 5
GDC_HUMAN
AC P16260: STANDARD: PRT; 332 AA.
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)

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Query Match	18.3%	Score 454.5	DB 1	Length 332
Best Local Similarity	36.0%	Pred. No. 1.1e-22		
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Grave's disease carrier protein (GDC) (Grave's disease autoantigen)			
DE	(GDA) (Mitochondrial solute carrier protein homolog).			
GN	SLC25A16 OR GDA.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Thyroid;			
RX	MEDLINE=90114217; PubMed=2575220.			
RA	Zarrilli R., Oakes E.L., McBride O.W., Lerman M.I., Chan J.Y.,			
RA	Santisteban P., Ursini M.V., Notkins A.L., Kohn L.D.;			
RT	"Sequence and chromosomal assignment of a novel cDNA identified by			
RT	immunoscreeing of a thyroid expression library: similarity to a			
RT	family of mitochondrial solute carrier proteins.";			
RL	Mol. Endocrinol. 3:1498-1508(1989).			
RN	[2]			
RP	REVISONS TO C-TERMINUS.			
RX	MEDLINE=93091248; PubMed=1457817;			
RA	Fiermonte G., Runswick M.J., Walker J.E., Palmeri F.;			
RT	"Sequence and pattern of expression of a bovine homologue of a human			
RT	mitochondrial transport protein associated with Grave's disease.";			
RL	DNA Seq. 3:71-78(1992).			
RN	[3]			
RP	FUNCTION, AND SUBCELLULAR LOCATION.			
RX	MEDLINE=21106356; PubMed=11158296;			
RA	Prohl C., Pelzer W., Dietert K., Kmitya H., Bedekovics T., Kisfal G.,			
RA	Lill R.;			
RT	"The yeast mitochondrial carrier Leu5p and its human homologue Graves'			
RT	disease protein are required for accumulation of coenzyme A in the			
RT	matrix.";			
RL	Mol. Cell. Biol. 21:1089-1097(2001).			
CC	-1- FUNCTION: Required for the accumulation of coenzyme A in the			
CC	mitochondrial matrix.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial			
CC	inner membrane.			
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.			
CC	-1- DISEASE: POSSIBLE ROLE IN GRAVES' DISEASE. THIS PROTEIN IS			
CC	RECOGNIZED BY IGG FROM PATIENTS WITH ACTIVE GRAVE'S DISEASE.			
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.			
CC	-1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 320			
CC	ONWARD DUE TO A FRAMESHIFT.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M31659; AAA36329.1; ALT_FRAME.			
DR	PIR; A40141; AA0141.			
DR	MIM; 139080; -			
DR	InterPro: IPR002067; Mit_carrier.			
DR	InterPro: IPR001993; Mitoch_carrier.			
DR	Plam; PF00135; mito_carr; 3.			
DR	PRINTS; PR00926; MITOCARRIER.			
DR	PROSITE; PS00215; MITOCH_CARRIER; 3.			
KW	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.			
FT	TRANSMEM 134 154 POTENTIAL.			
FT	TRANSMEM 191 211 POTENTIAL.			
FT	TRANSMEM 234 254 POTENTIAL.			
FT	REPEAT 1 123 1.			
FT	REPEAT 124 219 2.			
FT	REPEAT 220 332 3.			
SO	SEQUENCE 332 AA; 36235 MW; CFBDBFAF3E7F0F4B CRC64;			


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CC EMBL: M24103; AAA30769.1; -
DR PIR: B43646; B43646.
DR InterPro: IPR002067; Mit_carrier.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KM Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 2 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DF6EDE4061 CRC64;

Query Match 14.8%; Score 369; DB 1; Length 298;
Best Local Similarity 32.3%; Pred. No. 3.5e-17;
Matches 96; Conservative 62; Mismatches 111; Indels 28; Gaps 10;

OY 196 ROLLGGGAGVSRSTAPLDRLKIMOV-HGSK---SDKM--NIFGFRQWKEGIRS 249
DB 10 KDFLAGGIAAISKTAVALERKLLQYOHASKQIADKQYKGYDCIVRIPEGVLS 69
OY 250 LWRNGTNYIKIAPETAVFWAYEYKKLLTEEGOKIGTFEPIFGSM---AGATAQT 304
DB 70 FWRGNLANVIRFPQALNFAFKDKKQIFLGVDKRTQFWRFAFANLSSGAAAGATSLC 129
OY 305 FIYPMEMKTRLA--VGKTG---QYSGIYDCAKILKHEGLGAFYKGYVNLGIIIPYAG 359
DB 130 FVYPLDFARTRLAADVGKSGSEEREFGDCLVTKIRKSGIRGLYOGFVNSVOGIIITYRA 189
OY 360 IDLAVYELLSYWLDFNFAKDSVNPVGWVLGCGALLSTGQGLASYPALVTRFMQAQML 419
DB 190 ATEGVIDTRAK-----GMLDPKNTHTIVSWMIAQIYTAAGVSYSPDITRRRMMQSGR 244
OY 420 EGSPOL--NMVGLFRRIRISKEGIPGLYRITPFMKILPAVGISY--VYENKQOTL 472
DB 245 KGADIMYKGTVCQMKRIKDEGSKAFKGAMSN--VLNMGCAFVLVLYDELKAYI 298

RESULT 10
ADT3_HUMAN STANDARD; PRT; 298 AA.
ID A12336; 096C49;
AC 01-OCT-1988 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
DE (Adenine nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
ADP/ATP translocase."
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
```

```
RN [3]
RP SEQUENCE OF 36-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houdsworth J., Actardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC - FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC - SUBUNIT: HOMODIMER.
CC - SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC - DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC - SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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CC EMBL: J03592; AAA36750.1; -
DR PIR: B014775; AAH14775.1; -
DR PIR: S03894; S03894.
DR PIR: B28116; B28116.
DR MIM: 300151; -
DR MIM: 403000; -
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KM Mitochondrion: Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 100 1.
FT REPEAT 101 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 105 108 KHTQ -> RHA (IN REF. 3).
FT CONFLICT 242 242 S -> F (IN REF. 2).
SQ SEQUENCE 298 AA; 32866 MW; 18534E9F0EA9672F CRC64;

Query Match 14.8%; Score 368; DB 1; Length 298;
Best Local Similarity 32.7%; Pred. No. 4e-17;
Matches 97; Conservative 60; Mismatches 112; Indels 28; Gaps 10;

OY 196 ROLLGGGAGVSRSTAPLDRLKIMOV-HGSK---SDKM--NIFGFRQWKEGIRS 249
DB 10 KDFLAGGIAAISKTAVALERKLLQYOHASKQIADKQYKGYDCIVRIPEGVLS 69
OY 250 LWRNGTNYIKIAPETAVFWAYEYKKLLTEEGOKIGTFEPIFGSM---AGATAQT 304
DB 70 FWRGNLANVIRFPQALNFAFKDKKQIFLGVDKRTQFWRFAFANLSSGAAAGATSLC 129
OY 305 FIYPMEMKTRLA--VGKTG---QYSGIYDCAKILKHEGLGAFYKGYVNLGIIIPYAG 359
DB 130 FVYPLDFARTRLAADVGKSGSEEREFGDCLVTKIRKSGIRGLYOGFVNSVOGIIITYRA 189
OY 360 IDLAVYELLSYWLDFNFAKDSVNPVGWVLGCGALLSTGQGLASYPALVTRFMQAQML 419
DB 190 ATEGVIDTRAK-----GMLDPKNTHTIVSWMIAQIYTAAGVSYSPDITRRRMMQSGR 244
OY 420 EGSPOL--NMVGLFRRIRISKEGIPGLYRITPFMKILPAVGISY--VYENKQOTL 472
DB 245 KGADIMYKGTVCQMKRIKDEGSKAFKGAMSN--VLNMGCAFVLVLYDELKAYI 298
```

DB 245 KGADIMYTGVDWCWKIFRDEGGKAFKGAWSN---VLRMGGAFAVLVLYDELKRV 298

RESULT 11

LEU5_YEAST STANDARD: PRT: 357 AA.

AC P38702;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Mitochondrial carrier protein LEU5.

CN LEU5 OR YHR002W.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RA [1]

RP SEQUENCE FROM N.A.

RC STRAIN=S288C / AB972;

RX MEDLINE=94378003; PubMed=8091229;

RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favell A., Fulton L., Gallung S., Geisel C., Kirsten J., Kuuba T., Hillier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevisan E., Vaughan K., Vignati D., Wilcox L., Woldman P., Waterston R., Wilson R., Vaudin M.;

RA "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome VIII."

RT Science 265:2077-2082(1994).

RL [2]

RN FUNCTION, AND SUBCELLULAR LOCATION.

RX MEDLINE=21106356; PubMed=11158296;

RA Prohl C., Pelzer W., Diekert K., Knita H., Bedekovics T., Kispal G., Lill R.;

RA "The yeast mitochondrial carrier Leu5p and its human homologue Graves' disease protein are required for accumulation of coenzyme A in the matrix."

RT Mol. Cell. Biol. 21:1089-1097(2001).

CC -1- FUNCTION: Required for the accumulation of coenzyme A in the mitochondrial matrix.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

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CC -----

DR EMBL: U10555; AAB68424.1; -.

DR PIR: S46795; S46795.

DR SGD: S0001044; LEU5.

DR InterPro: IPR002067; Mit_carrier.

DR InterPro: IPR001993; Mitoch_carrier.

DR Pfam: PF00153; mito_carr; 3.

DR PRINTS: PR00926; MITOCARRIER.

DR PROSITE: PS00215; MITOCH_CARRIER; 3.

DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.

FT TRANSMEM 136 153 POTENTIAL.

FT TRANSMEM 208 228 POTENTIAL.

FT TRANSMEM 325 347 POTENTIAL.

FT SEQUENCE 357 AA; 40825 MW; 16266b2cd4b99605 CRC64;

Query Match 14.7%; Score 365; DB 1; Length 357;

Best Local Similarity 30.1%; Pred. No. 7.9e-17;

Matches 98; Conservative 55; Mismatches 123; Indels 50; Gaps 9;

OY 196 ROLLAGIAGAVSTRTSTPLDRKLTMMOV---HSGK--SDKNNIFGTRQWKEGCI 250

DB 35 RSLAGAGISGSCAKTFLIAPLRKIKILFQTSNPHYKTYGSLGLVEAKHIMWNGKGF 94

OY 251 WRNGNTNVIKIAPEFAVFWFAVEQYKKILTEEGCKIGTFERFISGSMGATQPIYME 310

DB 95 FQGHSAATLRLTFPVAVFAVFAVEQIRNLTIPSKEFESHMRRLVSGSLGCSVFITPLD 154

OY 311 VKRTLAAGKTQGYSGIYDCAKKILKEHGLGA-----FYKGYVBNLLGI 354

DB 155 LVRLVLAETEHRKRVKRLRIKKIKYEPASATLKNDYIPNMFCHMCNFRGYVPTVIGM 214

OY 355 IPYAGIDLAIVEL---LKSTW-----LDNFAKDSVNP-GVAVLGCGLS 395

DB 215 IPYAGVSFPAHLDLHDVYKSPFFAPYSLVLESDDELRVYKQRPPLRTMAELISGLLA 274

OY 396 STCGOLASVPLAVTRTRQAOAMLEGP-----OLNVGJFRRIISKE-GIPGLYRGT 448

DB 275 GNASOTPAVPEITIRRLQVSAV---SPKTYMDHKFOSISEIAHIIIFKRGYRGFFVGLS 331

OY 449 PNFMKVLPVAGISYVYENMKOTLCV 474

DB 332 IGYIKVTPMVACSFYVERMKWNGFI 357

RESULT 12

ADT2_MOUSE STANDARD: PRT: 298 AA.

ID ADT2_MOUSE

AC P51881; 061311;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE ADP, ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)

DE (Adenine nucleotide translocator 2) (ANT 2).

CN SLC25A5 OR ANT2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

RA [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=97059403; PubMed=8903724;

RA Ellison J.W., Li X., Francke U., Shapiro L.J.;

RA "Rapid evolution of human pseudautosomal genes and their mouse homologs."

RT Mamm. Genome 7:25-30(1996).

RL [2]

RN SEQUENCE FROM N.A.

RC TISSUE=Skeletal muscle;

RA Sheldon J.G.;

RA Thesis (1995), University of Cambridge, U.K.

RL [3]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SV;

RA Costet P., Laplace C.;

RA Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.

RL [4]

RP REVISIONS.

RA Laplace C.;

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RX PubMed=10974536;

RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;

RA "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes."

RL Gene 254:57-66(2000).

CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: HOMODIMER.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

```

CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch)).
CC -----
DR EMBL: U27316; AAC52838.1; -
DR EMBL: U10404; AAA19009.1; -
DR EMBL: X70847; CAA50196.1; -
DR EMBL: AF240003; AAF64471.1; -
DR MGD: MGI:1353496; SLC25A5.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SO SEQUENCE 298 AA; 32931 MW; 0798E04B987EFE20 CRC64;

Query Match 14.5%; Score 360; DB 1; Length 298;
Best Local Similarity 31.9%; Pred. No. 1.3e-16;
Matches 94; Conservative 60; Mismatches 113; Indels 28; Gaps 10;

QY 196 ROLLAGGAGVAVSRSTALDLRLKIMQV-HGSK---SRKM-NITGGRQWKEGIGTS 249
DB 10 KQFLAGGVAALSKTAVNAIEKVKLLQVQHASKQITADKQYKGIIDCVVRIRPEKGIVLS 69
QY 250 LKRGNTVNIKIAPETAVVAYVEYOYKRLTEEGOKIGTFEERFISGM-----AGATAQT 304
DB 70 FMRGNLIANVIRFPQALFAFKDKTKQJFLGCVDRKTFWIRFQNLASGCAAGATSLC 129
QY 305 FIYPMEVMTKRLA-VGKTG---QYSGIYDCAKKILKHGELGAFYKGYVNLGIIIPYAG 359
DB 130 FYYPIDFAFTRLADYGVKAGAEERFKGLDCLVYKIKSGDKGLVGFNVSVGGIITTYRA 189
QY 360 IDLAVYELLKSTWLDNFADSVNPGVMYLLGCGALSTGCGQLASTPLAVRTMRQAQML 419
DB 190 AVEGYIDTKA-----GMLDPKNTLHIFISWMAQSVTAVAGLSTPFEDVRRMMQSGR 244
QY 420 EESPOL--NMVGLFRRIRIKSGIPGLYRGITPFNMKVLPAVGISY--VYYENMKQ 470
DB 245 KETDLMYGTITLQWKRKIARDGSKAFKGMASN---VLGMGGAFLVLYDEIK 296

RESULT 13
ADT2_HUMAN STANDARD: PRT; 298 AA.
AC 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

```

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
RT cloning and sequence.";
RL J. Biol. Chem. 265:16060-16063(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated.";
RL J. Biol. Chem. 262:4355-4358(1987).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen C.N., Su Y., Baybayan P., Siruno A., Nagaraia R.,
RA Mazarella R.A., Schlessinger D., Chen E.Y.;
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Becker M., Graves T., Ozersky P.;
RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -!- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -!- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch)).
CC -----
DR EMBL: M57424; AAA51737.1; -
DR EMBL: J02683; AAA3579.1; -
DR EMBL: L78810; AAB39266.1; -
DR EMBL: AC004000; AAB96347.1; -
DR EMBL: J03591; AAA36749.1; -
DR PIR: A29132; A29132.
DR PIR: C28116; C28116.
DR MIM: 300150; -
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.

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Query Match	14.3%	Score 355.5	DB 1	Length 386
Best Local Similarity	31.2%	Pred. No. 3.6e-16		
Matches 92% Conservative	55	Mismatches 117	Indels 31	Gaps 7

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OY 188 EKKSGÖMRRÖLLAGIGIAAIVASTRTSTAPLDREIMMQVIGSKSDKM-----NIFG 236
Db 80 EKGFAAFNTDFLMGVSVAASVKTAAPLERVKLLQ-----NÖDEMLKAGRLSEPRKKGIGE 135
OY 237 GFRÖMVKCGGIRISLMRGCTNVIKTAPEYAKFMAV EGYKKILTEEGOKIGTEFRF---- 292
Db 136 CEGRIKCEEGGSSLMRGNTANVIRFPTÖALNFAFKDEYKRFLENKKPRDGGWKMFAGNL 195
OY 293 IGSAGACATQOFIYPMVMKTRLA---VCKTG---OYSGIYDCAKRIIHREGGAEYK 345
Db 196 ASGGAAGASSLEFFYSLDYARTRLNDRKASKKGGEROPNGILVDYKKTLSDSGIAGILYR 255
OY 346 GYVPLNGLIIFPAGIDIAVYELLLSKYWLDNFAKOSVNPGBVWVLGGCALISSTGOLASYP 405
Db 256 GFNISCVAIIYRGILFQMYDSIKPVLLTGNLÖDS----FFASFGILMWLITNGAGLASYP 311
OY 406 LALYTRMQÖQAMLEGSQPLNMWGLFRRRIISKEGIFGLYRGITTRPFMAYPLAVAGI 460
Db 312 IDIYARRRRMMNTSG-EAYAYKSSLDLFEISQIVKNEGKSLFKGGAAILPRAVAGAGV 365

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Search completed: August 18, 2002, 09:31:11
Job time: 486 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 09:22:25 ; Search time 69.46 Seconds

(without alignments)
1188.001 Million cell updates/sec

Title: US-09-777-921A-2

Perfect score: 2481

Sequence: 1 MLRWLRFALEPTACQDAEQ.....VGISVYVENKQTLGVTK 477

Scoring table:

BLOSUM62

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

SPTREMBL_19:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-rylous:*
16: sp-bacteriap:*
17: sp-archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2373	95.6	475	6	018757	018757 oryctolagus
2	2132	85.9	411	4	09P129	09P129 homo sapien
3	1518	61.2	473	11	09D565	09D565 mus musculu
4	1487	59.9	568	4	096P21	096P21 homo sapien
5	1397	56.3	484	4	096N04	096N04 homo sapien
6	1285	51.8	482	4	09BV35	09BV35 homo sapien
7	1110	44.7	311	4	09BSA6	09BSA6 homo sapien
8	902	36.4	370	5	09VTX3	09VTX3 drosophila
9	885.5	35.7	487	10	09F143	09F143 arabidopsis
10	852	34.3	479	10	09LY28	09LY28 arabidopsis
11	840	33.9	478	10	09FLS8	09FLS8 arabidopsis
12	652	26.3	631	3	09HE62	09HE62 neurospora
13	612.5	24.7	545	3	096US1	096US1 saccharomyc
14	521	21.0	352	10	004619	004619 arabidopsis
15	520	21.0	322	10	09F082	09F082 oryza sativ
16	520	21.0	332	10	09M058	09M058 arabidopsis

17	506	20.4	358	10	09M333	09M333 arabidopsis
18	500.5	20.2	426	3	094502	094502 schizosach
19	475	19.1	348	10	09SH98	09SH98 arabidopsis
20	462	18.6	126	11	099KD3	099KD3 mus musculu
21	455.5	18.4	415	10	09M024	09M024 arabidopsis
22	454.5	18.3	381	10	065023	065023 arabidopsis
23	448	18.1	316	5	09NI37	09NI37 trichomonas
24	448	18.1	325	10	09S219	09S219 arabidopsis
25	446	18.0	385	10	09ZNY4	09ZNY4 solanum tub
26	446	18.0	352	10	09S0V1	09S0V1 arabidopsis
27	445.5	18.0	381	10	09LD54	09LD54 oryza sativ
28	434.5	17.5	428	10	09LV81	09LV81 arabidopsis
29	429.5	17.3	294	5	093717	093717 caenorhabdi
30	425.5	17.2	418	10	09C9R4	09C9R4 arabidopsis
31	417.5	16.8	326	3	012251	012251 saccharomyc
32	410.5	16.5	377	5	09VDL7	09VDL7 drosophila
33	400.5	16.1	319	10	09MA27	09MA27 arabidopsis
34	371	15.0	298	13	09PRH1	09PRH1 rana rugosa
35	369	14.9	339	10	09EF73	09EF73 arabidopsis
36	368	14.8	298	13	09PRH2	09PRH2 rana rugosa
37	367.5	14.8	348	10	09LJX5	09LJX5 arabidopsis
38	367	14.7	298	13	09ITC4	09ITC4 rana rugosa
39	365	14.7	298	4	096C49	096C49 homo sapien
40	362.5	14.6	334	10	094222	094222 oryza sativ
41	360	14.5	298	13	09I9M9	09I9M9 xenopus lae
42	359	14.5	301	5	025692	025692 plasmodium
43	357.5	14.4	346	10	09LIF7	09LIF7 arabidopsis
44	356	14.3	301	5	026006	026006 plasmodium
45	355.5	14.3	315	4	09H0C2	09H0C2 homo sapien

ALIGNMENTS

RESULT	ID	1	PRELIMINARY;	PRT;	475 AA.
018757	018757				
AC	018757				
DT	01-JAN-1998 (TREMURel. 05, Created)				
DT	01-JAN-1998 (TREMURel. 05, Last sequence update)				
DE	01-DEC-2001 (TREMURel. 19, Last annotation update)				
DE	PEROXISOMAL CA-DEPENDENT SOLUTE CARRIER.				
OS	Oryctolagus cuniculus (Rabbit).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX	NCBI_TaxId=9986;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-97385133; PubMed-9238007;				
RA	Weber F.E., Minestrini G., Dyer J.H., Werdner M., Boffelli D.,				
RA	Compassi S., Wehrli E., Thomas R.M., Schultness G., Hauser H.;				
RT	"Molecular cloning of a peroxisomal Ca2+-dependent member of the				
RT	mitochondrial carrier superfamily."				
RL	Proc. Natl. Acad. Sci. U.S.A. 94:8509-8514(1997).				
CC	-1- SIMILARITY: TO OTHER EF-HAND CALCIUM BINDING PROTEINS.				
DR	EMBL; AF004161; AAB69156.1; -				
DR	HSSP; P09860; 3CTN				
DR	InterPro; IPR002048; EF-hand.				
DR	InterPro; IPR001993; Mitoch_carrier.				
DR	InterPro; IPR002067; Mlt_carrier.				
DR	Pfam; PF00036; efhand; 4.				
DR	Pfam; PF00153; mito_carr; 3.				
DR	PRINTS; PRO0926; MITOCARRIER.				
DR	SMART; SM0054; EFh; 3.				
DR	PROSITE; PS00018; EF_HAND; UNKNOWN_3.				
KW	Calcium-binding.				
SQ	SEQUENCE 475 AA; 53006 MW; E779D43F7C758269 CRC64;				

Query Match 95.6%; Score 2373; DB 6; Length 475;
Best Local Similarity 95.2%; Pred. No. 3.7e-170;
Matches 454; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

QY 1 MURWLDALPPLAACQDAEQPTRYETLFOALDRNGDVYDDELQEGRLNGLPIPGQDAE 60
DB 1 MURWLRGVLPLAACQGAEPPTRYETLFOALDRNGDVYDDELQEGRLNGLPIPGQDAE 60
QY 61 EKPIFTGVNKGKLDLFEFEMKYLKDHEKMKLAFKSLDKNDKNGKTEASEIYQSLOTGL 120
DB 61 EKPIFTGVNKGKLDLFEFEMKYLKDHEKMKLAFKSLDKNDKNGKTEASEIYQSLOTGL 120
QY 121 TISEQOAEILLQSIDVDGTMVDMNEMRDYFLFNPVTDEEIIIRPKHSTGIDIGSLTI 180
DB 121 TISEQOAEILLQSIDVDGTMVDMNEMRDYFLFNPVTDEEIIIRPKHSTGIDIGSLTI 180
QY 181 PDEFDEDEKKSQGMKOLLAGIAGAVSRTSTAPLDRKIMQVHGSKSDKNNIFGFRQ 240
DB 181 PDEFDEDEKKSQGMKOLLAGIAGAVSRTSTAPLDRKIMQVHGSKSDKNNIFGFRQ 238
QY 241 MKEGGSISLMNGTNTYIKIAPETAVKFMAVEQYKLLTEGOKIGTFERRISGSMAGA 300
DB 239 MKEGGSISLMNGTNTYIKIAPETAVKFMAVEQYKLLTEGOKIGTFERRISGSMAGA 298
QY 301 TAQPTIYMEVVKTRILAVKGTQOYSGIYDCAKKILKHEGLGAFYKGYVNLGIIPYAGI 360
DB 299 TAQPTIYMEVVKTRILAVKGTQOYSGIYDCAKKILKHEGLGAFYKGYVNLGIIPYAGI 358
QY 361 DLAVELLAKSYLDNFADKDSVNPVWLLCGALSTGQGLASYPLAVRTMQAQMLE 420
DB 359 DLAVELLAKSYLDNFADKDSVNPVWLLCGALSTGQGLASYPLAVRTMQAQMLE 418
QY 421 GSPOLNMVGLFRIISKEGIPGLYGTIPNFKVLPVAGISVYVENMKOTIGVOK 477
DB 419 GAPOLNMVGLFRIISKEGIPGLYGTIPNFKVLPVAGISVYVENMKOTIGVOK 475

RESULT 2
ID 09P129 PRELIMINARY: PRT: 411 AA.
AC 09P129.
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CALCIUM-BINDING TRANSPORTER (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=RETINA:
RA Biery B., Valle D.:
RT "Cloning and subcellular localization of a human calcium-binding
transporter."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF123303; AAF28888.1; -
DR HSSP: P09860; 3CTN.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR Pfam: PF00153; mito_carri_2.
DR PRINTS: PR00926; MITOCARRIER.
DR SMART: SM00054; EFh_3.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_3.
FT NON_TER 1
SQ SEQUENCE 411 AA; 45819 MW; 99A3B5BAD9C2A4CF CRC64;

Query Match 85.9%; Score 2132; DB 4; Length 411;
Best Local Similarity 99.8%; Pred. No. 4e-152;
Matches 409; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 FALPFAACQDAEQPTRYETLFOALDRNGDVYDDELQEGRLNGLPIPGQDAEKKFTTG 67
DB 1 FVLPLAACQDAEQPTRYETLFOALDRNGDVYDDELQEGRLNGLPIPGQDAEKKFTTG 60

QY 68 DVNKGKLDLFEFEMKYLKDHEKMKLAFKSLDKNDKNGKTEASEIYQSLOTGLTISEQDA 127
DB 61 DVNKGKLDLFEFEMKYLKDHEKMKLAFKSLDKNDKNGKTEASEIYQSLOTGLTISEQDA 120
QY 128 ELIIDSIDVDGTMVDMNEMRDYFLFNPVTDEEIIIRPKHSTGIDIGSLTIPEDETD 187
DB 121 ELIIDSIDVDGTMVDMNEMRDYFLFNPVTDEEIIIRPKHSTGIDIGSLTIPEDETD 180
QY 188 EKKSQGMKOLLAGIAGAVSRTSTAPLDRKIMQVHGSKSDKNNIFGFRQWKEGGI 247
DB 181 EKKSQGMKOLLAGIAGAVSRTSTAPLDRKIMQVHGSKSDKNNIFGFRQWKEGGI 240
QY 248 RSLMRNGTNTYIKIAPETAVKFMAVEQYKLLTEGOKIGTFERRISGSMAGATQFTLY 307
DB 241 RSLMRNGTNTYIKIAPETAVKFMAVEQYKLLTEGOKIGTFERRISGSMAGATQFTLY 300
QY 308 PNEVVKTRILAVKGTQOYSGIYDCAKKILKHEGLGAFYKGYVNLGIIPYAGIDLAVEL 367
DB 301 PNEVVKTRILAVKGTQOYSGIYDCAKKILKHEGLGAFYKGYVNLGIIPYAGIDLAVEL 360
QY 368 LKSYLDNFADKDSVNPVWLLCGALSTGQGLASYPLAVRTMQAQ 417
DB 361 LKSYLDNFADKDSVNPVWLLCGALSTGQGLASYPLAVRTMQAQ 410

RESULT 3
ID 09D5G5 PRELIMINARY: PRT: 473 AA.
AC 09D5G5.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 4930443612RIK. PROTEIN.
GN 4930443612RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawaji T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadohira K., Matsuda H. A., Ashburner M., Batalov S., Caaveant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
Kuehl P., Lewis S., Matsuo Y., Nakai I., Pesole G., Quackenbush J.,
Schraml L. M., Staahl F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,
Brownstein M. J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gastlisch S., Hill D., Hofmann M., Hume D. A., Kamliya M., Lee N. H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombauts P.,
Nortone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki K., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K. F.,
Suzuki H., Toyokawa K., Wang K. H., Weitz C., Whitaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AK015371; BAB29816.1; -
DR HSSP: O64537; 1DVI.
DR MGD: MGI:1921936; 4930443612RIK.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR Pfam: PF00153; mito_carri_3.
DR PRINTS: PR00926; MITOCARRIER.
DR SMART: SM00054; EFh_4.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_1.
SQ SEQUENCE 473 AA; 53375 MW; 6EF920A84651EB63 CRC64;

Query Match	Similarity	51.2%	Score 1518:	DB 11:	Length 473:
Best Local	Similarity	59.9%	Pred No. 7.5e-106:		
Matches 284;	Conservative	87;	Mismatches 101;	Indels	2;
					Gaps 2
OY	1	MLRWLDFALPFAACODAEQPRYETLFOALDRNGDVGVDIEGLEGNLIGPLGDAE	60		
DB	1	MLRLQDFLFLPSEACQNDVNRLAYEVLFDLHDNGGVVDITELRGLKHMMSLSEDE	60		
OY	61	EKIFITGGVKNCKGKLDLFEFPMYKLDHEKMKLAFLSLKNDNGKLEASLQSLTGL	120		
DB	61	KEIFMDADSMASGDLDFEEFVQYLODHEKMKLAFKSLDKNDGVIDASEIYAAVRSIGI	120		
OY	121	TSEGOAELILOSIDVGMATVDMMNWRPYFLFNPDTLDEIRLREKHSHTGIDIGSLT	180		
DB	121	HLSLQAKDILKSMDFSGMYDMDNMRQFFHFHAKNTDIDYRFKHSHTIIDIGISIT	180		
OY	181	PDETFEDEKKSQGMWRQLLAGSIAGAVSFTSAPLDRLKIMQVHGSKDKNIFEGFRO	240		
DB	181	PDEFEEQEKMSGEMMKRLVAAGIASAIFRTCTAPLERLKVTMQVSLKMKGLVHMFRO	240		
OY	241	MKEGGISLWNGNGNTVNIKIPETAVKRWAAEQYKKLLTEGOKITGETRFLSGMAA	300		
DB	241	MKEGGFSLWNGNVLNIKIPETAIKGAYEQYKKLLSFGDHLGVLDRTAGCMGA	300		
OY	301	TQATFYIPEMVKRTFLAVGKTGOYGIYCAKKILKEHGAFAFYKGYVNLGIIIPYGI	360		
DB	301	TSQTCVYPMREVTKTFLNLSKTEIGSYGLDVCYKLLKREIQAFSKGYVNLSTIIPYGL	360		
OY	361	DLAYELLKSYLWLNPAKDSVNPQWVLLGCGALSTCGQLASYPALVTRTMQADALE	420		
DB	361	DLTEILLKMHLEHYAGNSVNPGLAIVLGCTSHTCQLASFPLIVTRTMQA-VMLE	419		
OY	421	GSPOLNMVGLFRIISKEGIPGLYGIPIPNFKVLPVAGISVYVENMKOTIGV	474		
DB	420	KEYTRAMQLOIEITYTKBSKGFPGFTFNVLLKLPVAGISGVAHLYKRLFGL	472		
RESULT	4				
O96PZ1	PRELIMINARY:	PRT:	568 AA.		
AC	O96PZ1.				
DT	01-DEC-2001 (TREMBLrel. 19, Created)				
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)				
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE	KIA1896 PROTEIN (FRAGMENT).				
	KIA1896.				
	Homo sapiens (Human).				
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=BRAIN:				
RX	MEDLINE=21456161, PubMed=11572484;				
RA	Nagase T., Kikuno R., Ohara O.;				
RT	"Prediction of the coding sequences of unidentified human genes. XXI.				
RT	The complete sequences of 60 new cDNA clones from brain which code for				
RL	large proteins."				
RL	DNA Res. 8:179-187(2001).				
DR	EMBL, AB067483; BAB67789.1; -.				
FT	NON-TER				
SO	SEQUENCE	568 AA;	63578 MW;	81A02DCD8CEE7A4B8	CRC64;

	Query Match	Score 1487:	DB 4:	Length 568;
	Best Local Similarity	59.3%:	Pred. No. 2.1e-103:	
	Matches 276; Conservative	69;	Mismatches 72;	Indels 12; Gaps 1
Oy	61 EKIIPTGDVNNKGLDFFEEFMRYLDDHEKKMLAARSLDKRNDNGKTIEASIVOSTLTGL	120		
	: : : : : : : : : : : : : : : : :			
Db	140 KRIYAGGDDLDGGDLEEFEEFVHYLDQDHKEKLIVFRSLDRKNDRGIRDAEIMQSLLFDGV	199		

Oy	121	TISBQAEILIQSI-----	-DVDGIMYMDNMNDYELFENPVTDDEELIRWKH	168
Db	200	KISDQAEILIKRIPTGHWGVPYTMNDNIMTMDNMWRYHLHPVENPELITLYWKH		259
Oy	169	STGIDIGSLTPDEFTDEDEKSGQMROLLAGTAGAVSRTPAPLDRLKIMQVHGSK		228
Db	260	STIPFVGENLVPDEFTYEEHQTKGMMWHLVAGGAGAVSTCTAPLDRLKVLQMVASR		319
Oy	229	SDKNNIFEGFNQWKEGSIIRSLMRONGTNVIKIAPEYAKFMAVEOYKKLLTEEGQKIGT		288
Db	320	SNMNGIVGFTQMIREGARSLSMRGNGINVLKIAPESAIKFMAEQIKRLVGSQDEFLRI		379
Oy	289	PERFTSSMAGNTQOTFIYPMWKKTRALVAKTKOYQSYIYDCAKKILKHESLAFYGYV		348
Db	380	HERLVAGSLAGIAOSSIFYPMELIKTRALKRKTQYSGMLCDLRIAREVAAFYGYV		439
Oy	349	PALLGIIFYAGIDLAVLYELLSKSYMLDNPAKDSVNPVGWVLILGCGALSTGQSLASPLAL		408
Db	440	PMMLGIIFYAGIDLAVLYELTKLNNMLQHVAVNSADPGVYVLLAGCTMSTGQSLASPLAL		499
Oy	409	VFTRMQAOAMLEGSFOLNMVGLFPRRIISKEGIPGLYGTIPFMKVLPAVGISYVYENM		468
Db	500	VFTRMQAOASIEGAPETVMSLSFKHILRTGCAFGLRGCLAPFMKVLPAVISYVYENL		559
Oy	469	KQTLCVTKQK 477		
Db	560	KITLGVQSR 568		
RESULT	5			
O96NQ4		PRELIMINARY;	PRT; 384 AA.	
AC	O96NQ4:			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	CDNA FLJ30339 FTS, CLONE BRAC2007401, MODERATELY SIMILAR TO			
DE	ORCOTOLAGUS CUNICULUS PEROXISOMAL CA-DEPENDENT SOLUTE CARRIER			
DE	MRNA.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=CEREBLUM;			
RA	Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,			
RA	Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,			
RA	Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,			
RA	Kawai-Hiro Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,			
RA	Matsuo K., Nakamura Y., Sekine K., Kikuchi H., Kanda K., Nagatsuma M.			
RA	Kurakawa K., Kanehori K., Takahashi-Fuji A., Oshima A., Sugiyama A.,			
RA	Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuno Y., Nagai K.,			
RT	Isoeqal T.;			
RL	"NEDO human cDNA sequencing project.":			
RL	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.			
SR	EMBL; AK054901; BAB/0825.1; -			
SO	SEQUENCE 384 AA; 43018 MW; 33973A38D1P9BC5E CRC64;			

	Query Match Similarity	56.3%	Score 1397;	DB 4	length 384;
	Best Local Similarity	65.5%;	Pred. No. 6, 8e-97;		
	Matches	251; Conservative	68; Mismatches	64; Indels	0; Gaps
QY	95	FESLDKNNDKGLEASFIYVSLDTGLTITSEQAQLLDSIDVDGHTVTVMNEMWROYFLFN	154		
		: : : :			
Db	2	FPSLRPNODGHITDVSTIQOSFRALGISLSLEAEKLITMSDRGGTTIMDMGRHFFLIH	61		
		: : : :			
QY	155	PVTDIEETIRFKMKSHTGIDIGDLTIIPDEFTEDEKKSGGMROLLAGGTAGAVSRSTAP	214		
		: : : :			
Db	62	SLENEDVLIVFMKHSIVLDIGECTLVVPDFESSOEKRTGMMGVOLAVGAAGVASRGTAP	121		
		: : : :			

QY 215 LDRKIMOVHSGSKSDKMNIEGSGFROMYKEGIRSIMRNGNTNVIKIAPIETAVKEMAYEQ 274
DB 122 LDRLEFQOVHASKTNRLNIIIGLSRSMVEEGIRSLMRNGNTNVLKIAPESAIKEMAYEQ 181
QY 275 YKLLTLEEGOKIGTFERFISGSAGATAQTFIYPMEMKTRIAVKTGQSYIYCAKRI 334
DB 182 IKRALLGOQETLHVOERFVAGSLAGATAQTFIYPMELVLTRLTLKRTGYKGLLDCARKI 241
QY 335 LKHEGIGAFAFKGYVNPNLGIIIPYAGIDLAVALYELLKSYWLDNFKADSVNPGVAVLLGCGAL 394
DB 242 LEREPRAFYRGLYLPNVGLIIPYAGIDLAVALYETLKNWMLQOYSHDSADPGLIYLLACGTI 301
QY 395 STCGOLASYPALVYTRMGAQAMLEGSFOLNMVGLFRRIISKEGIPGLYRGITTPNEMKV 454
DB 302 STCGOLASYPALVYTRMGAQASIEGFPOLSMGLHRLHLSQEGMRGLYRGIAPIEMKV 361
QY 455 LPAVGISVYVENMKOTLGVTOK 477
DB 362 IPAVISIVYVENMKOALGVISR 384

RESULT 6
Q9BV35 PRELIMINARY: PRT: 482 AA.
AC Q9BV35: 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEICAL 54.0 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EYE, RETINOBLASTOMA;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC001656; AAH01656.1; -
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR001993; Mitoch_carrler.
DR InterPro: IPR002067; Mlt_carrler.
DR Pfam: PF00153; Mito_carr; 2.
DR PRINTS: PR00926; MITOCCARRIER.
DR SMART: SM00054; EFh. 3.
DR PROSITE: PS00018; EF_HAND; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 482 AA; 54035 MW; 8917BFA2BC2FE42B CRC64;

Query Match 51.8%; Score 1285; DB 4; Length 482;
Best Local Similarity 53.7%; Pred. No. 2.6e-88;
Matches 242; Conservative 77; Mismatches 78; Indels 54; Gaps 3;

QY 17 DAEOPTRETTLFOALDRNGDGVVDIGELQEGRNIGPLGQD---AEKITTGTDVYKD 72
DB 7 DAERORNGRLEFEELDSNKGDRVDVHELROGLARLG---GGNPDDGAOAGISSEGADEP 63
QY 73 GLDDEEFPKYLKDEHKMKLAFKSLDKNNKGKTEASEIYVOSTLQTLTSSQOAEILIQ 132
DB 64 GLDLDEESRKYLOERQORLLMFHSLDRNOGDHIDSEIQOSFRALGISTISLOAEKILH 123
QY 133 STDVDTMTVMNEMRWDFLFPVTDIEBILIRFKHST----- 170
DB 124 SMDRGTMTIDWQWRDHLHLSTLENVEDVLYFKHSTLSSAGFSAMIKDSTAEONRSKT 183
QY 171 -----GIDIGSLTIPDETTEDEKSGOMWOLLAGGTAG 205
DB 184 TYLARRSGSHLKSQHFGRPKWADHEVLIDIGELIYVDEFSSKOEKLTGMWKOVLAVGAVAG 243
QY 206 AVSRSTAPLDLKTIMOVHSGSKSDKMNIEGSGFROMYKEGIRSIMRNGNTNVIKIAPIET 265
DB 244 AVSRGTAPLDLKVFMQVHASKTNRLNIIIGLSRSMVEEGIRSLMRNGNTNVLKIAPIES 303

QY 266 AVKEMAYEQYKLLTLEEGOKIGTFERFISGSAGATAQTFIYPMEMKTRIAVKTGQYS 325
DB 304 ALKEMAYEQIKRALLGOQETLHVOERFVAGSLAGATAQTFIYPMELVLTRLTLKRTGYK 363
QY 326 GIYDCAKTLKHEGIGAFAFKGYVNPNLGIIIPYAGIDLAVALYELLKSYWLDNFKADSVNPGV 385
DB 364 GLDCAARRILEREPRAFYRGLYLPNVGLIIPYAGIDLAVALYETLKNWMLQOYSHDSADPGL 423
QY 386 NVLLGCGALSTCGOLASYPALVYTRMGAQ 416
DB 424 LVLLAGTISTTCGOLASYPALVYTRMGAQ 454

RESULT 7
Q9BSA6 PRELIMINARY: PRT: 311 AA.
AC Q9BSA6: 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEICAL 34.0 KDA PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE, RHABDOMYOSARCOMA;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; BC005163; AAH05163.1; -
DR InterPro: IPR001993; Mitoch_carrler.
DR InterPro: IPR002067; Mlt_carrler.
DR Pfam: PF00153; Mito_carr; 3.
DR PRINTS: PR00926; MITOCCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 311 AA; 33991 MW; 37F8E1B2684B3905 CRC64;

Query Match 44.7%; Score 1110; DB 4; Length 311;
Best Local Similarity 66.6%; Pred. No. 1.9e-75;
Matches 203; Conservative 51; Mismatches 51; Indels 0; Gaps 0;

QY 173 DIGDSLITPDETFTEDEKSGOMWOLLAGGIGAGVSRSTAPLDRLKIMOVHSGSKSDK 232
DB 7 DYGENLIVPDEFTVEERQOGMMRHILVAGGAGVSRCTAPLDRLKYLMOYHNASRNNM 66
QY 233 NIFGSGFROMYKKGIRSLMRNGNTNVIKIAPIETAVKEMAYEQYKLLTLEEGOKIGTFERF 292
DB 67 GLVGFTQMIIRRGARSLMRNGNTNVLKIAPIESAIKEMAYEQIKRLLYSGDQETLRINERT 126
QY 293 ISGSAGATAQTFIYPMEMKTRIAVKTGQYSGIYDCAKTLKHEGIGAFAFKGYVNPIL 352
DB 127 VAGSLAGATAQSSIYPMELVLTTRMALRKQGYSGMIDCARRILAEAGVAAFYKGYVNPIL 186
QY 353 GIIPAGTDLAYELLKSYWLDNFKADSVNPGVAVLLGCGALSTTCGOLASYPALVYTR 412
DB 187 GIIPAGIDLAVALYETLKNWMLQOYSHDSADPGLIYLLACGTISTTCGOLASYPALVYTR 246
QY 413 MOQAAMLEGSFOLNMVGLFRRIISKEGIPGLYRGITTPNEMKVLPVAGISVYVENMKOTL 472
DB 247 MOQAASIEGAPENVYSSLEKHLIRTEGARGLYRGLAPNEMKVIPAVISIVYVENNLKITL 306
QY 473 GVTOK 477
DB 307 GVOOSR 311
RESULT 8
Q9VTX3

ID 09VYX3 PRELIMINARY; PRT; 370 AA.
 DT 01-MAY-2000 (TReMBLrel_13, Created)
 DT 01-MAY-2000 (TReMBLrel_13, Last sequence update)
 DT 01-OCT-2001 (TReMBLrel_18, Last annotation update)
 DE CG4392 PROTEIN.
 GN CG4392.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY.
 RX MEDLINE=129196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mottman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Branton R.C., Rogers Y.-H.C., Blaziel R.G., Chame M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayan A., An H.-J., Andrews-Plankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Berson K.Y., Benos P.V., Bernick B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cayley S., Dahle C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fodler C., Gabriellian A.E., Gaig N.S., Gelbart W.M., Glasser K.,
 RA Foster G., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C.,
 RA Jallali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kraivit S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinelt K., Remington C.S., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spraker E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.W., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC EMBL: AEO03541; AAF49922.1; -;
 CC FLYBase: FBgn0036283; CG4392.
 DR InterPro: IPR001993; Mitoch.carrier.
 DR InterPro: IPR002067; Mit.carrier.
 DR Pfam: PF00153; mito carri; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH.CARRIER; 1.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SO SEQUENCE 370 AA; 41539 MW; 9AA41BA9A5E5CCE1 CRC64;

Query Match	36.4%	Score 902;	DB 5;	Length 370;
Best Local Similarity	53.4%;	Pred. No. 1.1e-59;		
Matches 182;	Conservative 58;	Mismatches 75;	Indels 26;	Gaps

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Db      MEDVEFVIRDMAGRIJLDIGEDMNPVDDTQEMQOTGLMRRLVAVGGIAGAVSRKCTAPLD      87
Qy      RLKIMQVHGSK---SDKMNIEGGFROVMEGGIRSLMRNGTNYKIAPEYAVKKWMAV      277
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Db      RIKVLYQVNOBPYVQOTORMGISCECHMILNDEGSGSRMWRNGINVLKIAPEYAFKFAAY      147
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Qy      EYKALL--TEBGOKITGFEEFPISSMAGATAPFIYMEVEMKRIPLAVGKQYSGIYDC      333
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Db      EOMKRLINGDDOSRMSIYERVAGAAAGGISOITIIYMEVLRKTRILRLRRGQYAGIADA      207
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Qy      AKKILHEGLAFYGYGVYNLLGIIPYAGIDLAVLEYELKSWLNFNAKDSVNPVAVMLG      390
      331
Db      AVKIKQGVASFNGVYVNLNIGLIPYAGIDLAVLEYELKRYIANH--DNNQPSFVYLLA      266
      208
Qy      CGAUSSTCGQLASVPLAVLVRTRMQAOAM-----LEGSP-----QLANVGLFRR      433
      331
Db      CGSSTSTJGOLCSYPLAVLVRTRLOAOAAEETIANOKRKTQIPLKSSDAHSGEETWTGLFRK      326
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Qy      IISKREGIPGLRGITPNPMKLVAVNGISVYVYEMNKOTGLV      474
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Db      IYRDGGLTGLRGITPNFLKLVPAVSISYVYETYSRLGLI      367
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RESULT	9			
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DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	CALCIUM-BINDING TRANSPORTER-LIKE PROTEIN.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	Eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=COLUMBIA;			
RX	MEDLINE=99397451; PubMed=10470850;			
RA	Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,			
RA	Miyajima N., Tabata S.;			
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. IX.			
RT	Sequence features of the regions of 1,011,550 bp covered by seventeen			
RT	pl and TAC clones."			
RL	DNA Res. 6:183-195(1999).			
DR	EMBL; AB017063; BAB08751.1; -			
DR	HSSP; P09860; 1F15.			
DR	InterPro; IPR002048; EF-hand.			
DR	InterPro; IPR001993; Mitoch_carrier.			
DR	InterPro; IPR002067; Mlt_carrier.			
DR	Pfam; PF00153; mltc_carr; 3.			
DR	PRINTS; PR00926; MITOCARRIER.			
DR	SMART; SM00054; Efh_2			
DR	PROSITE; PS00018; EF_HAND; UNKNOWN_1.			
DR	SEQUENCE; 487 AA; 54505 MW; 22688650C8841537 CRC64;			

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OY	19	EOPTRYETLFGALDRNGSDVDIGELQGLRNIGIPLGDAAEIKFTTGGVNRKDKLDFE	78			
Db	36	ERDRIIRLSFSPEDSENGYLDCAOIEEGKLCAIQIPSGKYAKLEFPVCADNARDGRVDA	95			
OY	79	EFMKYLRKHHEKKMLAFPSLDKNNGGKEASHIVGSLDTLGITTEQQOAEILGSDIVDG	138			
Dd	96	EFFRIMDDKELELYIFQAIDVENHGCSIPESLMDSLVKAGETIDEELARVEHVADKON	155			
OY	139	TMTVDNMNRDYFLFNP-VTDIEELIRFKWHSSTGDISDLTPDELFEEDEKSCWMRO	197			

Db 156 DGIIMEEWRDELLLYPHREATIENTENYHHMERVCLVDIGEOAVIPGEGISKHRSNYF--- 212
 Qy 198 LLAGAGIAGAVSRSTAPDLRLKIMMOVHGSKSDKMNIFEGFQOMYKEGIRSLMRNGNTN 257
 Db 213 -TAGGAGIAGASTATAPDLRLKVLQI--QKTD-ARIRAIKILIKOGVRGFRFGNGIN 268
 Qy 258 VIKIAPETAVKFWAYEQYKRL---LTEBGOKIGTFEERFISGSMAGATQFTIYPEVVK 313
 Db 269 IYKVAPESAIKFEYAYELFNAIGENMGEDKADIGTIVRLFAGMGAGAVQAOSTIPLDLVK 328
 Qy 314 TRL-----AVGKTGYSGIYDCAKKILKHEGAGFYKGYVNLGIIITPAGIDLAIV 364
 Db 329 TRLQYTSOAGVAVPRLGL-----KDLVHEGPRAYKGLFPLSLGIIIPYAGIDLA 382
 Qy 365 YELLKSYWLDNFPAKDSVNPVWVLLGCGALSTCGOLASYPALVTRMQAOAMLEGSPO 424
 Db 363 YETLNDLSSTYILQDA-EGGPLVQJGCGTISGALATCYVPIQVYTRMQAE-----RAR 436
 Qy 425 LNMVGLFRRITISKEGIPGLYRGITPNEKVLPAVGISYVYENMKOTL 472
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 AC Q9LY28;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
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 GN T211_30.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
 RA Rudd S., Lemcke K., Mayer K.F.X.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC -1- INNER MEMBRANE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AL163912; CAB67921.1; -.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001986; ESP_synthase.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR SMART; SM00054; EFh; 4.
 DR PROSITE; PS00104; EF_HAND; UNKNOWN_2.
 DR PROSITE; PS00104; ESP_SYNTHASE_1; UNKNOWN_1.
 DR PROSITE; PS00215; MITOCH_CARRIER; 1.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SEQUENCE 479 AA; 53969 MW; 38D58E1395316D6E CRC64;

Query Match 34.3%; Score 852; DB 10; Length 479;
 Best Local Similarity 39.4%; Pred. No. 9.3e-56;
 Matches 181; Conservative 90; Mismatches 172; Indels 16; Gaps 6;
 Qy 19 EGPTRYETLFOALDRNGGVVDIGELQELRLNGLIPGQDAEKKITTTGVNKKDKLDFE 78
 Db 33 EREIRIRSLDFPDNSNLGFLDYAQIEKGLASLQIPPEYKVARDLFRVCDANRDRGVYDQ 92
 Qy 79 EFMKTLKHHEKMKIAFASLKNNDGKITASEIVSLOTILGTLISEQAEILLQSIDVDG 138

Db 93 EFRRYIDAKELLYRIFQAIIDVHNCCILPEELMEALYAGIEIDDEELARVEVHDXDN 152
 Qy 139 IMTVNMENKRDYELNRP-VTDIEEIIIRFKHSTGIDIGSLIIPPEFDEKSGQMMRQ 197
 Db 153 NGTTFEEMRDFLLYPHEATIENTENYHHMERVCLVDIGEOAVIPGEGISKHRS---RL 208
 Qy 198 LLAGIAGAVSRSTAPDLRLKIMMOVHGSKSDKMNIFEGFQOMYKEGIRSLMRNGNTN 257
 Db 209 LLAGIAGAVSRSTAPDLRLKVLQVQRAHA---GVLPYIKIRREDKLMEGFRFGNGIN 265
 Qy 258 VIKIAPETAVKFWAYEQYKRL---LTEBGOKIGTFEERFISGSMAGATQFTIYPEVVK 316
 Db 266 IYKVAPESAIKFEYAYELFNAIGENMGEDKADIGTIVRLFAGMGAGAVQAOSTIPLDLVK 325
 Qy 317 -AVGKTGYSGIYDCAKKILKHEGAGFYKGYVNLGIIITPAGIDLAIVYELLKSYWLDN 375
 Db 326 TCYSEGGKAPKMKLTKDLVREGEPRAPYKGLFPLSLGIIIPYAGIDLAIVYELLKSLRY 385
 Qy 376 FAKDSVNPVWVLLGCGALSTCGOLASYPALVTRMQAOAMLEGSPOLNNGVLFRRII 435
 Db 386 ILQDT-EGGPLVQJGCGTISGALATCYVPIQVYTRMQAD-----SSKTYKQEFNMNTM 439
 Qy 436 SKEGIPGLYRGITPNEKVLPAVGISYVYENMKOTLGY 474
 Db 440 KEGGLRGFYRGLPLNLKLVPAASITYIYEAAMKSL 478

RESULT 11
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 AC Q9FLS8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PEROXISOMAL CA-DEPENDENT SOLUTE CARRIER-LIKE PROTEIN (PUTATIVE
 DE PEROXISOMAL CA-DEPENDENT SOLUTE CARRIER PROTEIN).
 GN MAC9.13.
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
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 RC STRAIN=COLUMBIA;
 RX MEDLINE=98290546; PubMed=9628582;
 RA Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. IV.
 RT Sequence features of the regions of 1,456,315 bp covered by nineteen
 RT physically assigned P1 and TAC clones.";
 RL DNA Res. 5:41-54(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
 RA Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
 RA Kosemura E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shim P.,
 RA Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RT "Full length cDNA of gene MAC9.13 (GI:10176874).";
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB010069; BAB10081.1; -.
 DR EMBL; AY056219; AAL07068.1; -.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR SMART; SM00054; EFh; 4.

[illegible]

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Db      7   QDRKVEELMTWKLDLPQKHGDELFEFGLOGLGRIRIDHPVFLVAQNMDHMLKDIKYNDTS    66
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Db      67  GDCKIQYEENFEFNPEVETAEEROLIMLFISIDRDKDGLRDLDNKRSAFOKAGITVSNKRLSGF    126
Oy      131  LOSTDVOCSTMTVDNNENNRDFLEFNPVD-----TEEIRPFKHSTGIDI -GDSL-    178
Db      127  FDEYDMHDGYISFDLENKDFLEMPHTNHNEHGHHASALEAALSFYSJIVYNAEGDSLIV    186
Oy      179  -----|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:    178
Db      187  SEPTLEGIGTGIFLLNMLFSGSLKLIASPGATTTPTSGSPAPDSKPSLSSPSSHYPDGTAE    246
Oy      179  -----TIDEFEEDKKSGQWRRQL-----|||:::|||||:|||||:|||||:|||||:    198
Db      247  PGAGANMAPSKIAPLVGATGPQVSADRAAHGOVYIKEMEGEGHDLROESDTSLKDEYVK    306
Oy      199  -----LAGGIAGAVSSTPAPLDRKIMMVOYGSKSDKM-----|||:::|||||:|||||:    233
Db      307  SGLTGLPLPDACYFLAAGVSSGVSTATAPLDRKLVELLVNTKRTTKTTYEAUKSQGPLSA    366
Oy      234  -----TFGGFROMVKEGGIRSLMRNGTNVIKIAETAFAKFWAYEQYKLLT-----E    281
Db      367  LRNMGCPITYDIRLMFRACGAKITEFFANGNLNVKIMPESAIRKSYEASKREFLAAYEGHN    426
Oy      282  EGOKIGFERIRISGSMGATGAQFIYMEWMKTRL-----AVGTGQYSGIYCAKILKH    337
Db      427  DPSQISTYSKVAVAGMGCMTRAQFCVFYITDLKFRLOCETVEYGPKGHALLIRAKNMWD    486
Oy      338  EGLGAFYKGVYNLLGITPYAGIDLAVELYLLKSYYLWNDFAK-----DSVNGCVNYLLGC    391
Db      487  GGLRAAYRGGLGLGILGMFEPSAIDIGTFEFLKSKYRKAAKYGVHEDDAAPGNVALGVL    546
Oy      392  GALSTCGQLASYPLALVRFRMQAQLBESSP-QLMNWGLFRILLKEGIPGLRYGILPN    450
Db      547  GASSGALGATVVYPLANLFRRLDTQGTAHPPYTGVADVAKTVRNIGIRGLYGLTPN    606
Oy      451  FMKVLPAGVISVYVENMKOTL_472
Db      607  LKVAPALSTHWCEYENMKITL_628

RESULT_13
O96US1 PRELIMINARY; PRT; 545 AA.
AC O96US1;
Dt 01-DEC-2001 (TrEMBLrel_19, Created)
Dt 01-DEC-2001 (TrEMBLrel_19, Last sequence update)
Dt 01-DEC-2001 (TrEMBLrel_19, Last annotation update)
DE YN1083W.
OS Saccharomyces cerevisiae (Baker's yeast).
CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_Taxid=4932;
RX MEDLINE=20439546; PubMed=10930523;
RX Belenkiy R., Haeffele A., Eisen M.B., Wohlrab H.;
"The yeast mitochondrial transport proteins: new sequences and
consensus residues, lack of direct relation between consensus residues
and transmembrane helices, expression patterns of the transport
protein genes, and protein-protein interactions with other proteins.",
Biochim. Biophys. Acta 1467:207-218 (2000).
LN [2]
RP SEQUENCE FROM N.A.
RA Belenkiy R., Wohlrab H.;
RL Submitted (SEP-2001) to the EMBL/Genbank/DDBJ databases.
DR EMBL; AF19344; AAL26493.1; -.
SO SEQUENCE 545 AA; 61270 MW; 8F3MA9AB392538E CRC64;
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DB 274 MCGWKDASAIIVTGEGRSTASLEYTGWADAFKRTVHHEGFGALYKGLVPSNVKVPSTAIATA 333
QY 462 YVYVENMKOTLGV 474
DB 334 FVYVENKDVLG 346

Search completed: August 18, 2002, 09:30:28
Job time: 483 sec

RESULT 15

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DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, last annotation update)
DE PUTATIVE PEROXISOMAL CA-DEPENDENT SOLUTE CARRIER PROTEIN.
GN P0019D06.21 OR P0024G09.9.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0019D06.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0024G09.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP002483; BAB16462.1; -;
DR EMBL; AP003311; BAB40117.1; -;
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_uncoupling.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; UNKNOWN.1.
SQ SEQUENCE 322 AA, 34876 MW, A649A692FBA6BD69 CRC64;

Query Match 21.0%; Score 520; DB 10; Length 322;
Best Local Similarity 40.5%; Pred. No. 4.7e-31;
Matches 117; Conservative 51; Mismatches 103; Indels 18; Gaps 7;

QY 198 LLAGGTAGAVSRSTAPDLRLKIMOVHGSKSP-----KMNIGGFRQMYKEGINSLSMR 252
DB 29 LAAGGFGAGAVSKTCTAPLRLTLTFQVAGHSDVAALKKYSIMHEASRIYREGEFGAFWK 88
QY 253 GNGTNYIKIAPFAVKKFWAEYOKKL-----LTREGQKIGTFERFISGSMAGATAQTFI 306
DB 89 GNLVTIVHRLPYSAISFYSTERKTKFLQRPVCGLDEDSNYGV-ARLLSGGLAGTTASVT 147
QY 307 YPMENKRTLAVGTQ-QYSGIYDCAKKILKHBGLGAFYGYVVPNLGIPYAGIDLAVY 365
DB 148 YPLDVVTRTLATQKTRRYKYGIFHAVSTICRDEGVKGLYGLGATLLGVGPSIAISFTYV 207
QY 366 ELLKSTYWLDFAKDSVNPQVMVLLGGCALSTGQLASTPLALVTRTRMQAMLEGSP-- 423
DB 208 ESLRSIMQMERPODS--PAVVSLSFS--GSLSGIASSTATFPLDLVKRRMQLQGAAGTSVC 264
QY 424 QLNMMVGLFRLLIKSGIPGLYRGITPMPKVLPAVGISYVYVENMKOTL 472
DB 265 KSSITGTIRQIFQKEGIRGFTYRGIVPEYLLKVPDSVGIAFTYETLSL 313

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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73: /cgn2_6/ptodata/1/pna/US6034_COMB.seq:*
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75: /cgn2_6/ptodata/1/pna/US6036_COMB.seq:*
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Print. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2673	100.0	2673	30	US-09-777-921-1
2	2519	94.2	3537	19	US-09-522-303-1193
3	2517.4	94.2	3545	25	US-09-649-163-8441
4	2517.4	94.2	3545	25	US-09-652-121-6793
5	2517.4	94.2	3545	25	US-09-652-123-9069
6	2517.4	94.2	3545	25	US-09-652-918-8162
7	2517.4	94.2	3545	26	US-09-667-617-1724
8	2517.4	94.2	3545	27	US-09-698-010-12652
9	2517.4	94.2	3545	28	US-09-710-285-1759
10	2517.4	94.2	3545	29	US-09-726-810-3387
11	2448	91.6	3446	60	US-60-213-360-3302
12	2448	91.6	3446	71	US-60-324-185-14440
13	2446.4	91.5	3393	56	US-60-172-360-23662
14	2446.4	91.5	3446	66	US-60-278-561-5850
15	2428	90.8	3384	1	PCT-US01-04098A-755
16	2096.2	78.4	3380	1	PCT-US01-14827-2497
17	2096.2	78.4	3380	22	US-09-577-408-3413
18	1347.6	50.4	2234	18	US-09-471-275-6014
19	1239.2	46.4	1280	25	US-09-644-869-8718
20	1239.2	46.4	1280	25	US-09-649-162-8703
21	1239.2	46.4	1280	25	US-09-652-127-8091
22	1135	42.5	6327	30	US-09-777-921-3
23	1059.6	39.6	3323	75	US-60-360-207-1516
24	954.6	35.7	1852	29	US-09-757-028-706
25	943.6	35.3	1090	34	PCT-US00-05882-54
26	943.6	35.3	1090	34	US-09-925-301-54
27	933.4	34.9	1839	17	US-09-359-922-4478
28	933.4	34.9	1839	17	US-09-359-922-4478
29	914.4	34.2	917	20	US-09-533-322-43
30	841	31.5	923	18	US-09-434-737-1544
31	841	31.5	923	32	US-09-850-118-1544

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OY	1621	ggagtgacttttctccctgaattcgaaacagctctatgcaaaagaagtcgattttt	1680
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Db	1741	cagaaatgttcaaaatcatatagattttaaattgtttgaaaaggccacaaattatatt	1800
OY	1801	tctttcttaataatccctgtaaaatccctctgcctgtaacccgaaatctgaaaatgctac	1860
Db	1801	tctttcttaataatccctgtaaaatccctctgcctgtaacccgaaatctgaaaatgctac	1860
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OY	2221	aatttcagatatactactgtttaaattaccacaacagaagaaattttggaagattccgt	2280
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OY	2281	ttatcctgcacatgtccttgaanaagcagcagaagaacgaatttttgaactgtatcagct	2340
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OY	2581	ggcgggggtgtatgacttctgaaaaacatgtgatccattttgaaaagggaaggcccaa	2640
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RESULT 2
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; Sequence 1193, Application US/09522303
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOCLEIC ACID MOLECULES DERIVED FROM A
; FILE REFERENCE: 1600.1086-001
; CURRENT APPLICATION NUMBER: US/09/522,303
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 60/123,393
; EARLIER FILING DATE: 1999-03-08
; NUMBER OF SEQ ID NOS: 1353
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1193
; LENGTH: 3537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-522-303-1193
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Db 698 ggataagcttaactatctccagatgaattcacaggaaagcaaaaaaaatccggacaatggt 727
QY 721 ggaagcagcttttggcagagagcattgtgtgtctctcgaacaagaactgtccctt 760
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QY 2521 ctttgaactgtctgtttgaataatgtggcagccacaaggaggagata 2567
Db 2556 ctttgaactgtctgtttgaataatgtggcagccacaaggaggagata 2602

RESULT 3
US-09-649-163-8441
; Sequence 8441, Application US/09649163
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Galvin, Katherine A.
; APPLICANT: Leiby, Kevin R.
; APPLICANT: Kingsbury, Gillian A.
; APPLICANT: Weich, Madeline S.
; APPLICANT: McCarthy, Sean A.
; APPLICANT: Williamson, Mark
; APPLICANT: Richardson, Jennifer
; APPLICANT: Macbeth, Kyle J.
; APPLICANT: Fraser, Christopher C.
; APPLICANT: Villeva, Jean-Luc M.G.

Db	1786	cagaaatggtccaaaatcatatggttttaatgtgtgtttgaaagggccacaaatataacttta	1845
Qy	1801	tctttcttaataatccctgcgcaaatctctgcgcctgaaatccgcaaatctgaaatgtactg	1860
Db	1846	tctttcttaataatccctgcgcaaatctctgcgcctgaaatccgcaaatctgaaatgtactg	1905
Qy	1861	ttgaaacaaattggtttgt	1920
Db	1906	ttgaaacaaattggtttgt	1965
Qy	1921	ttacgtttatgcagcttccctttatattttaaattctctgttttataattctgaaatg	1980
Db	1966	ttacgtttatgcagcttccctttatattttaaattctctgttttataattctgaaatg	2025
Qy	1981	tatgatttctttaaatttcccttatagtagaacccattaaagaaatcattacatttaaata	2040
Db	2026	tatgatttctttaaatttcccttatagtagaacccattaaagaaatcattacatttaaata	2085
Qy	2041	taccttcagcaaaaagatcccaataagatagatgggtttgtgccttattcttcctgc	2100
Db	2086	taccttcagcaaaaagatcccaataagatagatgggtttgtgccttattcttcctgc	2145
Qy	2101	tgaatcagaaatgaaacagatgtgtgtgaaattctgaaagggaagtatgaaatataattat	2160
Db	2146	tgaatcagaaatgaaacagatgtgtgtgaaattctgaaagggaagtatgaaatataattat	2205
Qy	2161	tcaaattggcagctttccatttaccatttaccatatttggttccgtgagtttaacact	2220
Db	2206	tcaaattggcagctttccatttaccatttaccatatttggttccgtgagtttaacact	2265
Qy	2221	aatttccaagatatactagttaataattaccacaagaagcaatttatttgaaagaattccgt	2280
Db	2266	aatttccaagatatactagttaataattaccacaagaagcaatttatttgaaagaattccgt	2325
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Qy	2401	ttatgctcaagaaagactctcttgggagccattcttaagtaactcgtaaattctttttaa	2460
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Qy	2461	atgaagtcggaattatcatatgacgaagatgagatgggcttatattctccctcaactgtgaatc	2520
Db	2506	atgaagtcggaattatcatatgacgaagatgagatgggcttatattctccctcaactgtgaatc	2563
Qy	2521	ctttgaaactgcgtgtttgcaatatatggcgagccacaaagggggagagata	2567
Db	2564	ctttgaaactgcgtgtttgcaatatatggcgagccacaaagggggagagata	2610
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: Sequence 6793, Application US/09652121			
: GENERAL INFORMATION:			
: APPLICANT: Distafo, Peter			
: TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES			
: TITLE OF INVENTION: THEOREM			
: FILE REFERENCE: 1600.1188-001			
: CURRENT APPLICATION NUMBER: US/09/652,121			
: PRIOR FILING DATE: 2000-08-30			
: PRIOR APPLICATION NUMBER: 60/151,129			
: PRIOR FILING DATE: 1999-08-30			
: NUMBER OF SEQ. ID NOS: 7615			
: SOFTWARE: FastSeq for Windows Version 4.0			
: SEQ. ID NO 6793			
: LENGTH: 3545			
: TYPE: DNA			
: ORGANISM: Homo sapiens			

US-09-652-121-6793									
Query Match 94.2%; Score 2517.4; DB 25; Length 3545;									
Best Local Similarity 99.3%; Pred. No. 0;									
Matches 2549; Conservative 0; Mismatches 16; Indels 2; Gaps 2;									
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Db	46	ccgcacaccgcagcgccgcccccaacgcgctgtgcgccgcgccgccccgacgcgcgcct	105						
Qy	61	gcgcgctgccgcgtctcgccccgcgcgcctcgatctccgttactctctgcgcagcgcg	120						
Db	106	gcgcgctgccgcgtctcgccccgcgcgcctcgatctccgttactctctgcgcagcgcg	165						
Qy	121	ccctgcgcctctgggacacatgttgcctctgctctgctggagacttcgcgcctgcgccacgcgcgt	180						
Db	166	ccctgcgcctctgggacacatgttgcctctgctctgctggagacttcgtctgcgccacgcgcgt	225						
Qy	181	gccaaagccgagagacgcgcgcctcagaaacccctctccaggcaactggacgcgaatg	240						
Db	226	gccaaagccgagagacgcgcgcctcagaaacccctctccaggcaactggacgcgaatg	285						
Qy	241	ggagacggagctggctggacatcggcgcgcctgcagggagcgctcagaaacctggcatccctc	300						
Db	286	ggagacggagctggctggacatcggcgcgcctgcagggagcgctcagaaacctggcatccctc	345						
Qy	301	tgggccaaagacgcgcgagagaaaattttactactggagatgtcaacaaagtgggaagc	360						
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Qy	361	tgagattctgaaagattcttgaaagtaccttaagaccatggagagaaatgaaattggcat	420						
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Qy	661	ggagatagcttaactatccacagatgaatticacggaaagacgaaaaaaatccgcgacaatggt	720						
Db	706	ggagatagcttaactatccacagatgaatticacggaaagacgaaaaaaatccgcgacaatggt	765						
Qy	721	ggagagcaactcttggcagagggcgatctgctgtgctgctctctcgaaacagacatgcccct	780						
Db	766	ggagagcaactcttggcagagggcgatctgctgtgctgctctctcgaaacagacatgcccct	825						
Qy	781	tgagaccgctgtgaaaaatctgatcgcggttccacggttccaacatccagacaaaatgacacat	840						
Db	826	tgagaccgctgtgaaaaatctgatcgcggttccacggttccaacatccagacaaaatgacacat	885						
Qy	841	ttggttgctcttcgcacagatgttaaaaagagagatccgcctgcctcttggaggggaatg	900						
Db	886	ttggttgctcttcgcacagatgttaaaaagagagatccgcctgcctcttggaggggaatg	945						
Qy	901	gtacaaacgtcatcaaaaaattgctctctggagacgctgttaaatcttggggcataatgacagt	960						
Db	946	gtacaaacgtcatcaaaaaattgctctctggagacgctgtgttaaatcttggggcataatgacagt	1005						
Qy	961	acaaagattactactgaagaagacaaaaaattggagacatttggagatttattcttg	1020						

Db 1006 acaagaagtlactactgaagaagacaaaatagacacatttgagatttctg 1065
Qy 1021 gtccatgtcgagcaactcgcagactttatatccaatgtaggtttgaaaaca 1080
Db 1066 gtccatggtcgagcaactcgcagactttatatccaatgtaggtttgaaaaca 1125
Qy 1081 ggtcgctgttagcaaaactcgagactctcgagatatagattgttccaagaaactt 1140
Db 1126 ggtcgctgttagcaaaactcgagactctcgagatatagattgttccaagaaactt 1185
Qy 1141 tgaacaatgaaggttggagcttttaacaaagctatgttcccaatttaagttaca 1200
Db 1186 tgaacaatgaaggttggagcttttaacaaagctatgttcccaatttaagttaca 1245
Qy 1201 taccttagcagcagatagatttctgtgtatgttagctttgaagcctattggcgtgata 1260
Db 1246 taccttagcagcagatagatttctgtgtatgttagctttgaagcctattggcgtgata 1305
Qy 1261 attttgcaaaaagactctgtlaaaccttgagtcagtgtctgtgagatcggtgcttat 1320
Db 1306 attttgcaaaaagactctgtlaaaccttgagtcagtgtctgtgagatcggtgcttat 1365
Qy 1321 ccagcaccgtgtgtccagctgtgccaagctacccatgtgcttggtagaacctcgcatgtcagg 1380
Db 1366 ccagcaccgtgtgtccagctgtgccaagctacccatgtgcttggtagaacctcgcatgtcagg 1425
Qy 1381 ctcaagcactgttagaaggttcccaagcgtcgaatatgttggcgtcttcttgaagcaata 1440
Db 1426 ctcaagcactgttagaaggttcccaagcgtcgaatatgttggcgtcttcttgaagcaata 1485
Qy 1441 ttcccaagaagaagaaataccaaagactttacagaaggcatcaccacaaacttcaagaagctgc 1500
Db 1486 ttcccaagaagaagaaataccaaagactttacagaaggcatcaccacaaacttcaagaagctgc 1545
Qy 1501 tccctgtctgttagcagtcagttaagtgtttatgaaaataatgaagcaaaactttagagtaa 1560
Db 1546 tccctgtctgttagcagtcagttaagtgtttatgaaaataatgaagcaaaactttagagtaa 1605
Qy 1561 ccagcaaatgtgtgttcactttttgtccttagcctgataatgaaactttcaaacactcct 1620
Db 1606 ccagcaaatgtgtgttcactttttgtccttagcctgataatgaaactttcaaacactcct 1665
Qy 1621 ggaatgtactttctcctcgaatctgaaacaagctcatgtgcaaaaagactgcatttttt 1680
Db 1666 ggaatgtactttctcctcgaatctgaaacaagctcatgtgcaaaaagactgcatttttt 1725
Qy 1681 cacaagaaggagaagcgttaacaatgttcaacttcaaaactttgggctaaatatatgtaca 1740
Db 1726 cacaagaaggagaagcgttacaatgttcaacttcaaaactttgggctaaatatatgtaca 1785
Qy 1741 cagaagaatgttcaaaatcatagtttaagtgtttgaaaaggccacaacaattatattactta 1800
Db 1786 cagaagaatgttcaaaatcatagtttaagtgtttgaaaaggccacaacaattatattactta 1845
Qy 1801 tcttttcttaataatcctcgcgaatctcgcctgaatccgaatctgaaaatgttactgac 1860
Db 1846 tcttttcttaataatcctcgcgaatctcgcctgaatccgaatctgaaaatgttactgac 1905
Qy 1861 ttgagaacaattgttctgtgtgtatagatataaatacatcaatccttattctgggtgtgt 1920
Db 1906 ttgagaacaattgttctgtgtgtatagatataaatacatcaatccttattctgggtgtgt 1965
Qy 1921 ttaagcttagcagcagctcttatatttaattctgttttatatatattgaaatgtctt 1980
Db 1966 ttaagcttagcagcagctcttatatttaattctgttttatatatattgaaatgtctt 2025
Qy 1981 tatagatttctttaaatcttccctta tagaacatlaaataagaaatcatlacatttaataa 2040
Db 2026 tatagatttctttaaatcttccctta tagaacatlaaataagaaatcatlacatttaataa 2085
Qy 2041 taccttagcagaaagcatccaataatagtagaggtttaagtcttattttcttccagc 2100
Db 2086 taccttagcagaaagcatccaataatagtagaggtttaagtcttattttcttccagc 2145

Qy 2101 tgaatacgaatgaacaagctgtgtgaatttctgaagggaagtgatgaanaattattatt 2160
Db 2146 tgaatacgaatgaacaagctgtgtgaatttctgaagggaagtgatgaanaattattatt 2205
Qy 2161 tcaagtgagcactttccattttacacactgttacatatttggttccctgaggtatataact 2220
Db 2206 tcaagtgagcactttccattttacacactgttacatatttggttccctgaggtatataact 2265
Qy 2221 aatttcagtatatactgtttaaataattacacaacaagaagcaattatttgaagatccgt 2280
Db 2266 aatttcagtatatactgtttaaataattacacaacaagaagcaattatttgaagatccgt 2325
Qy 2281 ttatcttccatgtgtttgaaaagcagcaggaagaaatttttgaactgtataoact 2340
Db 2326 ttatcttccatgtgtttgaaaagcagcaggaagaaatttttgaactgtataoact 2385
Qy 2341 ctgcagaagcacttctgtttctcctgttccctgttcttacccttttgaatcagatccgt 2400
Db 2386 ctgcagaagcacttctgtttctcctgttccctgttcttacccttttgaatcagatccgt 2445
Qy 2401 tttagtcagaagacttcttggagcactcttagtaaaccttgaatcttcttttaattgtc 2460
Db 2446 tttagtcagaagacttcttggagcactcttagtaaaccttgaatcttcttttaattgtc 2505
Qy 2461 atgaagtgatgatcatcagcagcagcagtgatgagccttatttccctcactgttgataatc 2520
Db 2506 atgaagtgatgatcatcagcagcagcagtgatgagccttatttccctcactgttgataatc 2563
Qy 2521 cttagaactgtctgttccaatatatgtgcagccacaagaaggagagaga 2567
Db 2564 cttagaactgtctgttccaatatatgtgcagccacaagaaggagagagata 2610

RESULT 5
US-09-652-123-9069
; Sequence 9069, Application US/09652123
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NOCTERIC ACID MOLECULES AND USES
; FILE REFERENCE: 1600.1186-001
; CURRENT APPLICATION NUMBER: US/09/652,123
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,135
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 9796
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9069
; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-652-123-9069

Query Match 94.2%; Score 2517.4; DB 25; Length 3545;
Best Local Similarity 99.3%; Pred. No. 0; Mismatches 16; Indels 2; Gaps 2;
Matches 2549; Conservative 0;
Qy 1 ccgaaccccgacgagcgcgcccaaacgctgtttgcgcgcgcgcgcgcgcgcgcgcgc 60
Db 46 ccgaaccccgacgagcgcgcccaaacgctgtttgcgcgcgcgcgcgcgcgcgcgcgc 105
Qy 61 ggcgtgtcccggtctgc 120
Db 106 ggcgtgtcccggtctgc 165
Qy 121 cctgcgcctcggagcactgttgcgcgtgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 180
Db 166 cctgcgcctcggagcactgttgcgcgtgtgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 225
Qy 181 gccagagcgcgagc 240

Db	226	gcccgaagcgcgagcagcgcgaacgcgcgtacgagacccctcttcaggcatctggaccgcaatg	285
QY	241	ggagccgagatgctgtagacatccgcgcgagcctgcgaagagggctcagagaaactgtagctcc	300
Db	286	ggagccgagatgctgtagacatccgcgcgagcctgcgaagagggctcagagaaactgtagctcc	345
QY	301	tgagccgagagccgagagagaaaaattttactactctgagatgtcaaaaaagtgggaac	360
Db	346	tgagccgagagccgagagagaaaaattttactactctgagatgtcaaaaaagtgggaac	405
QY	361	tgagatcttgaaagaatttatgaaatgtaaccttaagaagccatgagaaagaaatgtgacat	420
Db	406	tgagatcttgaaagaatttatgaaatgtaaccttaagaagccatgagaaagaaatgtgacat	465
QY	421	ttagagatttagacaaaaataatgataggaaaaaatgagcttcagaaattgcccagcttc	480
Db	466	ttagagatttagacaaaaataatgataggaaaaaatgagcttcagaaattgcccagcttc	525
QY	481	tcacgaacactgagctgtactacattctcgaaacaaacgaagcttgattcttcgaagcatg	540
Db	526	tcacgaacactgagctgtactacattctcgaaacaaacgaagcttgattcttcgaagcatg	585
QY	541	atgttgatggagacaatgacagctgagctggaatgaaatgagagactactcttaataac	600
Db	586	atgttgatggagacaatgacagctgagctggaatgaaatgagagactactcttaataac	645
QY	601	ctgttacaagacattggaagaaattatccgcttctcggaaacattctacagaatttgacag	660
Db	646	ctgttacaagacattggaagaaattatccgcttctcggaaacattctacagaatttgacag	705
QY	661	ggagatacctaactatctccagatgaaatctcaacggaagacgaaaaaaatcccgacaatggt	720
Db	706	ggagatacctaactatctccagatgaaatctcaacggaagacgaaaaaaatcccgacaatggt	765
QY	721	ggagagcagcttcttgacgagagcgatctgcgtgctgtctcctgaaacagcactgcccct	780
Db	766	ggagagcagcttcttgacgagagcgatctgcgtgctgtctcctgaaacagcactgcccct	825
QY	781	tgagccctctcgaaatatatgatactgagcttccacggttcaaaaatacgaacaaatgaaacat	840
Db	826	tgagccctctcgaaatatatgatactgagcttccacggttcaaaaatacgaacaaatgaaacat	885
QY	841	ttgtgtgcttctcgacagatgtaaaagaagggatctccgcctcgcttctggagaggaaatg	900
Db	886	ttgtgtgcttctcgacagatgtaaaagaagggatctccgcctcgcttctggagaggaaatg	945
QY	901	gtacaaaagctatcaaaaatgtgctccctcggaacagctatlaattctcggagatagaacgt	960
Db	946	gtacaaaagctatcaaaaatgtgctccctcggaacagctatlaattctcggagatagaacgt	1005
QY	961	acaaagaagttactactctgaaagaagagcaaaaaataggaacatttgaagattattctg	1020
Db	1006	acaaagaagttactactctgaaagaagagcaaaaaataggaacatttgaagattattctg	1065
QY	1021	gttccatgagctggagacacgtgcacacactttatatatccaatggaagtttagaaacaa	1080
Db	1066	gttccatgagctggagacacgtgcacacactttatatatccaatggaagtttagaaacaa	1125
QY	1081	ggctgctgttagagaaaaactgggacgactctgaaataatgatatgtgtccaaagaagatt	1140
Db	1126	ggctgctgttagagaaaaactgggacgactctgaaataatgatatgtgtccaaagaagatt	1185
QY	1141	tgaaacatgaaagctctggagagcttcttacaagaagctatgttcccaatttataggtatca	1200
Db	1186	tgaaacatgaaagctctggagagcttcttacaagaagctatgttcccaatttataggtatca	1245
QY	1201	tacctatgacgagatagactctgcgtgtgatgagctcttgaaagccctaatgtgcggatga	1260
Db	1246	tacctatgacgagatagactctgcgtgtgatgagctcttgaaagccctaatgtgcggatga	1305
QY	1261	attttgcaaaagatctctgtaaacctctgagatcattggttctgtagatgcggtgccttat	1320
Db	1306	attttgcaaaagatctctgtaaacctctgagatcattggttctgtagatgcggtgccttat	1365

QY	131	131	cagacccctgtgtgcagctcgcagctaccacattggtcttgttgaaactcgcgtcagc	1380
Db	1366	1366	ccagacacctgtgtgcagctcgcagctaccacattggtcttgttgaaactcgcgtcagc	1425
QY	1381	1381	ctcaagccatgttgaagaggtccccaagctbaatatgttgcgcctcttcagcaaat	1440
Db	1426	1426	ctcaagccatgttgaagaggtccccaagctbaatatgttgcgcctcttcagcaaat	1485
QY	1441	1441	ttcccaagaagaaataccagacatttaagagcgtacccccaaacttcataagctgc	1500
Db	1486	1486	ttcccaagaagaaataccagacatttaagagcgtacccccaaacttcataagctgc	1545
QY	1501	1501	ttccctgtctgtagatcatagttatgtgtttatgaaaatatgtagaacatttagagtaa	1560
Db	1546	1546	ttccctgtctgtagatcatagttatgtgtttatgaaaatatgtagaacatttagagtaa	1605
QY	1561	1561	cccagaaatgtatgttgcatttttgccttagcctgtataatgaacttcacaacacct	1620
Db	1606	1606	cccagaaatgtatgttgcatttttgccttagcctgtataatgaacttcacaacacct	1665
QY	1621	1621	ggagtgaccttttctcctcgaaatggaacaaagctatgtgcagaagaagctgcattttt	1680
Db	1666	1666	ggagtgaccttttctcctcgaaatggaacaaagctatgtgcagaagaagctgcattttt	1725
QY	1681	1681	cacaaaggaagaaagcgttaacaaatgttcactccaacttttgggttaattatgtaca	1740
Db	1726	1726	cacaaaggaagaaagcgttaacaaatgttcactccaacttttgggttaattatgtaca	1785
QY	1741	1741	cagaatgttccaatcatcatgcttttaattgttcttgtaaaagccacaaatataactta	1800
Db	1786	1786	cagaatgttccaatcatcatgcttttaattgttcttgtaaaagccacaaatataactta	1845
QY	1801	1801	tcttttcttaataactcctgcgaacactctgcgcctgaaatcccgaaatctgaaatgtactgc	1860
Db	1846	1846	tcttttcttaataactcctgcgaacactctgcgcctgaaatcccgaaatctgaaatgtactgc	1905
QY	1861	1861	ttgaaacaaattggtttgtgtgtgttagagtttaaacatcaacttaacttcgggggtgt	1920
Db	1906	1906	ttgaaacaaattggtttgtgtgtgttagagtttaaacatcaacttaacttcgggggtgt	1965
QY	1921	1921	ttaagttatgtccggttcccttatacttaataattctgtttatataatttgaatgtcct	1980
Db	1966	1966	ttaagttatgtccggttcccttatacttaataattctgtttatataatttgaatgtcct	2025
QY	1981	1981	tatagattctttraaattcttcctatagaacccattatagaanaatcatatcatatnaaata	2040
Db	2026	2026	tatagattctttraaattcttcctatagaacccattatagaanaatcatatcatatnaaata	2085
QY	2041	2041	tacttcaagaaagaaagatccaataatagatgggtttgtgccttatatttcttcgcgc	2100
Db	2086	2086	tacttcaagaaagaaagatccaataatagatgggtttgtgccttatatttcttcgcgc	2145
QY	2101	2101	tgaatacgaatgaaacacagctgtgtggaattctctgaagggaagtatgaaatataattat	2160
Db	2146	2146	tgaatacgaatgaaacacagctgtgtggaattctctgaagggaagtatgaaatataattat	2205
QY	2161	2161	tcaatgtggcacttttccatttaccacctgtacacattatttgtttccgtgagtataaact	2220
Db	2206	2206	tcaatgtggcacttttccatttaccacctgtacacattatttgtttccgtgagtataaact	2265
QY	2221	2221	aatttcaagatatactgttataattacacaaacaaaggaatttttgaagaattccgt	2280
Db	2266	2266	aatttcaagatatactgttataattacacaaacaaaggaatttttgaagaattccgt	2335
QY	2281	2281	ttatctgtccattgtcttggaaaagcagcaggaagaaatcttctgactgttatcagct	2340
Db	2326	2326	ttatctgtccattgtcttggaaaagcagcaggaagaaatcttctgactgttatcagct	2385
QY	2341	2341	ctgcaagcgcattcttgttcttcttctgttccctgttcttactctttgatacaagattccgt	2400
Db	2386	2386	ctgcaagcgcattcttgttcttcttctgttccctgttcttactctttgatacaagattccgt	2445

QY 2401 ttatgcagaagaactcttcttggaacatctcttagtaacctgaanaattcttctttaatctgc 2460
|||||
Db 2446 ttatgcagaagaactcttcttggaacatctcttagtaacctgaanaattcttctttaatctgc 2505
QY 2461 atgaagtgatgatcatatgagcaagtatgagcttattcttccctcaactgtgtgaatc 2520
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Db 2506 atgaagtgatgatcatatgagcaagtatgagcttattcttccctcaactgtgtgaatc 2563
QY 2521 ctctgaactgtctgttgcaatatgagcagcaanaaggggagagaga 2567
|||||
Db 2564 ctctgaactgtctgttgcaatatgagcagcaanaaggtgagagaga 2610

RESULT 6
US-09-652-918-8162
; Sequence 8162, Application US/096552918
; GENERAL INFORMATION:
; APPLICANT: Galvin, Katherine
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1187-001
; CURRENT APPLICATION NUMBER: US/09/652,918
; CURRENT FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/151,130
; PRIOR FILING DATE: 1999-08-30
; NUMBER OF SEQ ID NOS: 8985
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8162
; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-652-918-8162

Query Match 94.2%; Score 2517.4; DB 25; Length 3545;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2549; Conservative 0; Mismatches 16; Indels 2; Gaps 2;

QY 1 ccggaaccccgagcgcccccacaacgctgttgcgcgcgccgcccgcagccgcgctc 60
Db 46 ccggaaccccgagcgcccccacaacgctgttgcgcgcgccgcccgcagccgcgctc 105
QY 61 ggcgtgtcccggtctgcgcccgcagccctcgatctcccggtactctctggccaaggcg 120
Db 106 ggcgtgtcccggtctgcgcccgcagccctcgatctcccggtactctctggccaaggcg 165
QY 121 cctgcgctcttggaacatgttgcgctgctgcgggaacttcgcgctgcacccgcgctc 180
Db 166 cctgcgctcttggaacatgttgcgctgctgcgggaacttcgcgctgcacccgcgctc 225
QY 181 gccagagcgaggagcagcgagcagccttcccaagcacttgagccgcaatg 240
Db 226 gccagagcgaggagcagcgagcagccttcccaagcacttgagccgcaatg 285
QY 241 gggagcgaagtgtgacaatcgcgagctgcgaggggagcctgaaggaacttgacccctc 300
Db 286 gggagcgaagtgtgacaatcgcgagctgcgaggggagcctgaaggaacttgacccctc 345
QY 301 tgggcccagagcgcgagagagaanaatttactacttgagatgtcaacaanaagtggaaagc 360
Db 346 tgggcccagagcgcgagagagaanaatttactacttgagatgtcaacaanaagtggaaagc 405
QY 361 tggatattgaagaattatgaatgaacttaagaacatgagaagaanaattgaattgcat 420
Db 406 tggatattgaagaattatgaatgaacttaagaacatgagaagaanaattgaattgcat 465
QY 421 ttaagagtttagacaanaataatgagaanaattgaggtctcagaanaattgcagtttc 480
Db 466 ttaagagtttagacaanaataatgagaanaattgaggtctcagaanaattgcagtttc 525
QY 481 tccagacactgtgtcactattcttgacacacaagcagagttgattctcaaaagcatg 540
|||||

Db 526 tccagacactgtgtcactattcttgacacacaagcagagttgattctcaaaagcatg 585
QY 541 atgttgatggagcaatgagcagtgagcttgaaatgagagacacttctattatc 600
Db 586 atgttgatggagcaatgagcagtgagcttgaaatgagagacacttctattatc 645
QY 601 ctgttacagacattgaggaanaattatccgcttcttggaacacattctcaagaaattgacag 660
Db 646 ctgttacagacattgaggaanaattatccgcttcttggaacacattctcaagaaattgacag 705
QY 661 gggatagcttaactatcccaatgaaatccaaggaacgaaaaaattccggacaattgt 720
Db 706 gggatagcttaactatcccaatgaaatccaaggaacgaaaaaattccggacaattgt 765
QY 721 ggaagcaacttttgcaagagagcattgtcgtgtcgtctcttgaaacagcattgcccct 780
Db 766 ggaagcaacttttgcaagagagcattgtcgtgtcgtctcttgaaacagcattgcccct 825
QY 781 tggaccgtctgaaatctcatgatgatgcaggttcaacgattcaacaacatgacaatat 840
Db 826 tggaccgtctgaaatctcatgatgatgcaggttcaacgattcaacaacatgacaatat 885
QY 841 ttgtgtgcttcgacagatggttaaaagagagatccgcgtcgtcttgaggggaaatg 900
Db 886 ttgtgtgcttcgacagatggttaaaagagagatccgcgtcgtcttgaggggaaatg 945
QY 901 gtacaaacgtatcaaaatgtctcttgagacagcgtttaaattctcgggatatgaaagt 960
Db 946 gtacaaacgtatcaaaatgtctcttgagacagcgtttaaattctcgggatatgaaagt 1005
QY 961 acaagaagttaacttaactaagaagagacaaaataatgagaacatttgagattattctg 1020
Db 1006 acaagaagttaacttaactaagaagagacaaaataatgagaacatttgagattattctg 1065
QY 1021 gtccatggtctgagcaactgcacagacttataatccaaatgaggttatgtaaaacca 1080
Db 1066 gtccatggtctgagcaactgcacagacttataatccaaatgaggttatgtaaaacca 1125
QY 1081 ggcgtgtctgagcaaaactggtgcagctactcggaaatatatgtgtgccaaagaagatt 1140
Db 1126 ggcgtgtctgagcaaaactggtgcagctactcggaaatatatgtgtgccaaagaagatt 1185
QY 1141 tgaacatgaaaggtcttgagagcttcttcaaaaggtatgttcccaattattagatatca 1200
Db 1186 tgaacatgaaaggtcttgagagcttcttcaaaaggtatgttcccaattattagatatca 1245
QY 1201 taacttatgcagcatalagatcttgctgtgtatgagcctctgaaatgagcttatgtctgata 1260
Db 1246 taacttatgcagcatalagatcttgctgtgtatgagcctctgaaatgagcttatgtctgata 1305
QY 1261 attttgcaaaagattctgttaaaccctctgagatcatgtgtctgagatgagcttctat 1320
Db 1306 attttgcaaaagattctgttaaaccctctgagatcatgtgtgttgagatgagcttctat 1365
QY 1321 ccagacactgtgtgtagctctgagcagctacccacttgagcttggtaggaactgcagtcag 1380
Db 1366 ccagacactgtgtgtagctctgagcagctacccacttgagcttggtaggaactgcagtcag 1425
QY 1381 ctcaagcattgttagaaggttcccaacagctgaaatagttgtgacctcttctgacgaatga 1440
Db 1426 ctcaagcattgttagaaggttcccaacagctgaaatagttgtgacctcttctgacgaatga 1485
QY 1441 ttccaaagaaggaatlaccaaggaacttacaagagacatacccccaactcatgaaggtgc 1500
Db 1486 ttccaaagaaggaatlaccaaggaacttacaagagacatacccccaactcatgaaggtgc 1545
QY 1501 tccctgtctgtagcactcaggtatgtgtttagaanaataatgagaanaacttagagatga 1560
Db 1546 tccctgtctgtagcactcaggtatgtgtttagaanaataatgagaanaacttagagatga 1605
QY 1561 cccagaaatgattgtgcatattttgtcttagcctgataattgaacttcaacaactctc 1620
Db 1606 cccagaaatgattgtgcatattttgtcttagcctgataattgaacttcaacaactctc 1665

Db 826 tggacgctctgaaatacatatgatgcaggttccaggttccaaatacagacaataatgacacatat 885
Qy 841 ttgttggtcttcagacagatggttaaaagaaggtatccgcgtctgtgaggggaaatg 900
Db 886 ttgttggtcttcagacagatggttaaaagaaggtatccgcgtctgtgaggggaaatg 945
Qy 901 gtacaaacgtcatcaaaaattgctctctgagacagctgtttaaattctctgggcataatgacagt 960
Db 946 gtacaaacgtcatcaaaaattgctctctgagacagctgtttaaattctctgggcataatgacagt 1005
Qy 961 acaagaagttactactactgaagaagaagacaataataggaacctttgagaagattattctctg 1020
Db 1006 acaagaagttactactactgaagaagaagacaataataggaacctttgagaagattattctctg 1065
Qy 1021 gtccacgtgctgagcaactctcacagactttatataatccatgaggttatgaaacca 1080
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Db 1126 ggtctgctgttagcaaaaacttgggagctactcttggaatatatgaltgtgtccagaagaatt 1185
Qy 1141 tgaaccttgaaggtctgtggagctttttacaaaggtatgttcccaatttatagttatca 1200
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Qy 1201 tactttatgcagcatagatcttgcgtgtatgtagctcttgaaagttccattgtgctgata 1260
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Qy 1261 attttgcaaaaagatctctgtataaacctctggagtcagtgctgtgagatgagctctat 1320
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Qy 1621 gggagtgaactttctcctcgtgaattgaaacaagtcataatgcaaaagagctgcatctttt 1680
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Db 1786 cagaagaatgttcaaatcatagtttataatgtgttttgaagaaggccacaacttaactactta 1845
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Db 1846 tcttttcttaataatctctgcaaatctctgcctgaaatccgaaatctgaaaaatgtactgagc 1905
Qy 1861 ttgagaacaaattgtttgtgtgttagagttataaatcatataacttatttctgggtgagc 1920
Db 1906 ttgagaacaaattgtttgtgtgttagagttataaatcatataacttatttctgggtgagc 1965

Qy 1921 ttacgtttatgcccagttcccttataattaaatttctgttttataatatttgaatgtctt 1980
Db 1966 ttacgtttatgcccagttcccttataattaaatttctgttttataatatttgaatgtctt 2025
Qy 1981 tatagatttctttaaattctctctatagaaacattataagaataatcatattaaata 2040
Db 2026 tatagatttctttaaattctctctatagaaacattataagaataatcatattaaata 2085
Qy 2041 tactttacagaanaaggttccaaataagttataggtttatgttcttatttttcttcagc 2100
Db 2086 tactttacagaanaaggttccaaataagttataggtttatgttcttatttttcttcagc 2145
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Qy 2161 tcaagtggagacttttccatttaccactgtaccattatttggctctggagttatacact 2220
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Qy 2221 aattttcaagtatatctgtttaaatttaccacacaaaggcaatttattgaaagattccgt 2280
Db 2266 aattttcaagtatatctgtttaaatttaccacacaaaggcaatttattgaaagattccgt 2325
Qy 2281 ttatccctgcattgtcttgaagaagcagcaggaagaacgaatttttgaactgtatcagctt 2340
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Qy 2341 ctgcagagcatcttctgttctcctgttctgttcttcttaccatttgaatcagattccgt 2400
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Db 2446 tttagtcaagaagaacttcttgggacattctttagtaaccttgaatttttctttaaattgc 2505
Qy 2461 atgaagtgagattgtatcatgagcaagtgagtggtcttatttctccctcactgtgtgaatct 2520
Db 2506 atgaagtgagattgtatcatgagcaagtgagtggtcttatttctccctcactgtgtgaatct 2563
Qy 2521 ctltgaactgtgttctgcaatatgtggcagccacaagaagggtgagaga 2567
Db 2564 ctltgaactgtgttctgcaatatgtggcagccacaagaagggtgagaga 2610

RESULT 8
US-09-698-010-12652
; Sequence 12652, Application US/09698010
; GENERAL INFORMATION:
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: NOVEL NOCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.2029-001
; CURRENT APPLICATION NUMBER: US/09/698, 010
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 60/162,358
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 15684
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12652
; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-698-010-12652

Query Match 94.2%; Score 2517.4; DB 27; Length 3545;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2549; Conservative 0; Mismatches 16; Indels 2; Caps 2;
Qy 1 ccgcaccccgagcgcgcccaaacgtgtgtgcgcgcgcgcgcgcgcgcgcgcgcgcgc 60

[illegible]

Dd	1126	gqcgvgcgtfagagcaaaacacgggcagfctactctcgaaababafgattgicgcagaagaagattt	1185
Qy	1141	tgaacaacgaaagctctvggagccttlttacaagaagctatgttcccaattattatggtatca	1200
Dd	1186	tgaacaacgaaagctctvggagccttlttacaagaagctatgttcccaattattatggtatca	1245
Qy	1201	tactctatgcagagatagactctgcgtgtatagagctcttgaagccctatttgctgcgagata	1260
Dd	1246	tactctatgcagagatagactctgcgtgtatagagctcttgaagccctatttgctgcgagata	1305
Qy	1261	attttgcaaaagatctctgtaaacccctcgagatcaatgtgtctgcgagatgcgctctat	1320
Dd	1306	attttgcaaaagatctctgtaaacccctcgagatcaatgtgtctgcgagatgcgctctat	1365
Qy	1321	ccagacacttvgfctacgctctgscagacttaccatttgctcttggtagaactctgcaltgcag	1380
Dd	1366	ccagacacttvgfctacgctctgscagacttaccatttgctcttggtagaactctgcaltgcag	1425
Qy	1381	ctcaagcactgttgaagaggtctcccaacagctgatatgtgttgccctcttcgcagcaatla	1440
Dd	1426	ctcaagcactgttgaagaggtctcccaacagctgatatgtgttgccctcttcgcagcaatla	1485
Qy	1441	ttcccaagaagaagataccagagacttacaagagcacaaccccaactctatgaaggtgc	1500
Dd	1486	ttcccaagaagaagataccagagacttacaagagcacaaccccaactctatgaaggtgc	1545
Qy	1501	tccctgcgttgaagatcaagfctatgtgttatgaaatcttgaagaacactttagagatga	1560
Dd	1546	tccctgcgttgaagatcaagfctatgtgttatgaaatcttgaagaacactttagagatga	1605
Qy	1561	cccgagaaatgatgtgtcatcttcttgctcttgaacctgataatgtaaacttccaacactct	1620
Dd	1606	cccgagaaatgatgtgtcatcttcttgctcttgaacctgataatgtaaacttccaacactct	1665
Qy	1621	ggagtgacttcttctcctctgaatttgaaagaatgctatgtgcagaagaagctgacttttt	1680
Dd	1666	ggagtgacttcttctcctcctgaatttgaaagaatgctatgtgtgcagaagaagctgacttttt	1725
Qy	1681	cacaaagaggagacggttgaacaaatgtgtcacttcaaaccttctggtctaaatfatatgtca	1740
Dd	1726	cacaaagaggagacggttgaacaaatgtgtcacttcaaaccttctggtctaaatfatatgtca	1785
Qy	1741	cagaaatgcttcaaatcatcatagttttaatgtgtttgaaagaagccacaaatfatacttta	1800
Dd	1786	cagaaatgcttcaaatcatcatagttttaatgtgtttgaaagaagccacaaatfatacttta	1845
Qy	1801	tcttctcttaatactctctgtaaaatctcctcctcgaaatccgaaatcttgaaatgtactgctc	1860
Dd	1846	tcttctcttaatactctctgtaaaatctcctcctcgaaatccgaaatcttgaaatgtactgctc	1905
Qy	1861	ttgaaacaaatgtgttctgtgtgtgtgtgaagttaaaatcaatcaatcttattcgggtgtc	1920
Dd	1906	ttgaaacaaatgtgttctgtgtgtgtgtgaagttaaaatcaatcaatcttattcgggtgtc	1965
Qy	1921	ttaagttatagcaggtccttcttataatttcaattctctgtttatataatttggatgctt	1980
Dd	1966	ttaagttatagcaggtccttcttataatttcaattctctgtttatataatttggatgctt	2025
Qy	1981	tatagattctcttinaaatttcccttatagaacaaatgaagaatcaattatataattnaaata	2040
Dd	2026	tatagattctcttinaaatttcccttatagaacaaatgaagaatcaattatataattnaaata	2085
Qy	2041	tactctacagcaaaaagcatcccaaaataagatagtggtttatgtgccttatattcttcttcagc	2100
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Qy	2101	tgaataagatgaacacagacggtgtgaaattctcgaagaggaagtgatgaaatfatatttt	2160
Dd	2146	tgaataagatgaacacagacggtgtgaaattctcgaagaggaagtgatgaaatfatatttt	2205
Qy	2161	tcaatgvgacacttttccatttcaacacgtgaccatatttggcttccggagttataaact	2220
Dd	2206	tcaatgvgacacttttccatttcaacacgtgaccatatttggcttccggagttataaact	2265

QY	221	aalltcagatatactggttaataatccacaagaagcaatttatgtgaagaattccgt	2280
Db	226	aatttcagatattactgttaataatccacaagaagaatttatgtgaagaattccgt	2325
QY	2281	ttatccctgcattgctttgaaaaagcagcagcaagaagaaatttttgcctgtatcaagct	2340
Db	2326	ttatccctgcattgctttgaaaaagcagcagcaagaagaattcccttgcctgtatcaagct	2385
QY	2341	ctgcagaagcaactctgtttttccctgttcccttggttccactcttgcataagaattccgt	2400
Db	2386	ctgcagaagcaactctgtttttccctgttcccttggttccactcttgcataagaattccgt	2445
QY	2401	tttagtcagaagaagactctcttgggaccattcttagtaacctgaaattctttttcaattgc	2460
Db	2446	tttagtcagaagaagactctcttgggaccattcttagtaacctgaaattctttttcaattgc	2505
QY	2461	atgaagtgcattgacatgacatgagaagtgcattgccttattctccctcaactggtgaatc	2520
Db	2506	atgaagtgcattgacatgacatgagaagtgccttattctccctcaactggtgaatc	2563
QY	2521	cttgcgaactgctggtttgcaatatggtgcagccacaaagggtgagaga	2567
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RESULT 9
US-09-710-285-1759
: Sequence 1759, Application US/09710285
: GENERAL INFORMATION:
: APPLICANT: Geating, David P.
: APPLICANT: Donovan, Michael J.
: APPLICANT: Holtzman, Douglas A.
: TITLE OF INVENTION: NOVEL NOCLEIC ACID MOLECULES AND USES
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 1600-2006-001
: CURRENT APPLICATION NUMBER: US/09/710,285
: CURRENT FILING DATE: 2000-11-10
: PRIOR APPLICATION NUMBER: 60/164,507
: PRIOR FILING DATE: 1999-11-10
: NUMBER OF SEQ ID NOS: 2347
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 1759
: LENGTH: 3545
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-710-285-1759

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[illegible]

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DB	346	tgggccagagacgcccagagagaaaattttactactgagatgccaacaaagtgggaagc	405
QY	361	tggaatttgaaagaatttatgaaagtaacttaagaacacatgagaagaatagaattggcat	420
DB	406	tggaatttgaaagaatttatgaaagtaacttaagaacacatgagaagaatagaattggcat	465
QY	421	ttaaagatttgacaanaaaatgaatgaaagaaattgaagcttcagaatatgccaagcttc	480
DB	466	ttaaagatttgacaanaaaatgaatgaaagaaattgaagcttcagaatatgccaagcttc	525
QY	481	tcacagacacgcggtcgcactactctcgaacacaagaagatgtaattcttcaagaatg	540
DB	526	tcacagacacgcggtcgcactactctcgaacacaagaagatgtaattcttcaagaatg	585
QY	541	atgtttgatagggaacaatacgaatgagatcggaataatggagagagatcttcttaatac	600
DB	566	atgtttgatagggaacaatacgaatgagatcggaataatggagagagatcttcttaatac	645
QY	601	ctgttaacagacatctgaggaataatccggtttccggaacatctcaagaattggacag	660
DB	646	ctgttaacagacatctgaggaataatccggtttccggaacatctcaagaattggacag	705
QY	661	gggaatagctttaactactccagatgaattcagacggaagacgaaaanaaatccggaacat	720
DB	706	gggaatagctttaactactccagatgaattcagacggaagacgaaaanaaatccggaacat	765
QY	721	ggagagcagcttttggcagagagacatgctgctgctctcgcgaacagacatgcctct	780
DB	766	ggagagcagcttttggcagagagacatgctgctgctctcgcgaacagacatgcctct	825
QY	781	tggaagcgcgtgaaaaatcaatgaatgacgtttccagcttccaataacagacaaaatgaacat	840
DB	826	tggaagcgcgtgaaaaatcaatgaatgacgtttccagcttccaataacagacaaaatgaacat	885
QY	841	ttgtgtgctttccgacagatggttaaagaagaaagtaatccgcgcgctttgaaagggaaatg	900
DB	886	ttgtgtgctttccgacagatggttaaagaagaaagtaatccgcgcgctttgaaagggaaatg	945
QY	901	gtacaacacgtcatcaaaaattgtctcctcgaagacagctgttaaatctcgggcatagaacgt	960
DB	946	gtacaacacgtcatcaaaaattgtctcctcgaagacagctgttaaatctcgggcatagaacgt	1005
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DB	1006	acaaagaagttactactacgaaagaagacgcaaaaaatgaaacattttagagattattcttg	1065
QY	1021	gttccatgagctggagacacgcgcacacactttatataccaattggaagttatgaanaacca	1080
DB	1066	gttccatgagctggagacacgcgcacacactttatataccaattggaagttatgaanaacca	1125
QY	1081	ggctgagctgtgaagcaaaaactgggcagtaactcgaatatatagatgtgcgcaagaagattt	1140
DB	1126	ggctgagctgtgaagcaaaaactgggcagtaactcgaatatatagatgtgcgcaagaagattt	1185
QY	1141	tgaaacactgaagggcttggagggctttttaaagaagcagatgttcccaatttatagtatca	1200
DB	1186	tgaaacactgaagggcttggagggctttttaaagaagcagatgttcccaatttatagtatca	1245
QY	1201	tacactatgacagatagatcctgcgtgtatatagactcttgaaagcccatgtgcgcgata	1260
DB	1246	tacactatgacagatagatcctgcgtgtatatagactcttgaaagcccatgtgcgcgata	1305
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DB	1306	atttttgcaaaaagattctgtaaacctggaagtaatgttctgtcgtggatgcggtgcttat	1365
QY	1321	ccagacacctgtgtgcagctcggccaagctaccocatgtgcttggttgagaactcgcatgcag	1380
DB	1366	ccagacacctgtgtgcagctcggccaagctaccocatgtgcttggttgagaactcgcatgcag	1425
QY	1381	ctcaagcataltttgaaggtctcccaacacgtaaatgtgttgccctcttccaacaaatla	1440

Db	1426	ctcaagccacgtctgaaggtgtccccaagcgtcaatctgtgtgccccttcctgcagcaatta	1485
Oy	1441	ttcccaagaagagatccccaagacttaccagagcaccacccaactctcaagagctgc	1500
Db	1486	tttccaaagaagagataccagagacttaccagagcaccacccaactctcaagagctgc	1545
Oy	1501	tcctctcgttaggcacgaatgctgtgtttaagaataatgaagcaaaccttaaggataa	1560
Db	1546	tcctcctcgttaggcacgaatgctgtgtttaagaataatgaagcaaaccttaaggataa	1605
Oy	1561	cccgagaatgttgttgcattttttgttcgcttgatgttaataacttcaaacctcct	1620
Db	1606	cccgagaatgttgttgcattttttgttcgcttgatgttaataacttcaaacctcct	1665
Oy	1621	ggagtgacttttctccctgaatttgaacaacgctctggcaaaaagcgtgacttttt	1680
Db	1666	ggagtgacttttctccctgaatttgaacaacgctctggcaaaaagcgtgacttttt	1725
Oy	1681	cacaaaaggagaagcagtgtaacaatggtcaccttcaaaccttggcgctaattatagtca	1740
Db	1726	cacaaaaggagaagtggttaacaatggtcaccttcaaaccttggcgctaattatagtca	1785
Oy	1741	cagaaatgttcaaatatcatgcttttaatgtgtttgaaaaagccacaaattatacttta	1800
Db	1786	cagaaatgttcaaaaatcatgctttttaaagtggtttgaaaaagccacaaattatacttta	1845
Oy	1801	tctttctttaaatacctcgtcaaatctcgcctcgaaatccgaaatctgaanaatgtactgc	1860
Db	1846	tctttctttaaatacctcgtcaaaaatctcgcctcgaaatccgaaatctgaanaatgtactgc	1905
Oy	1861	ttgaacaaaatttgttttgtgtgttagagtgtaaaatcatcttatttcgggtgt	1920
Db	1906	ttgaacaaaatttgttttgtgtgttagagtgtaaaatcatcttatttcgggtgt	1965
Oy	1921	tttaagttatggccagttcccttattttaattcttgtttatatatttgaagtcct	1980
Db	1966	tttaagttatggccagttcccttattttaattcttgtttatatatttgaagtcct	2025
Oy	1981	tatagattctctttaaatttcccttatagaacocattaagaanaatcatfacatttaaaata	2040
Db	2026	tatagattctctttaaatttcccttatagaacocattaagaanaatcatfacatttaaaata	2085
Oy	2041	taccttaacgaaaaagcaccacaataagataaggtttatgtccttattttcttcagc	2100
Db	2086	taccttaacgaaaaagcaccacaataagataaggtttatgtccttattttcttcagc	2145
Oy	2101	tgaatacgaatgtaacaacagtggtgtgaaatttctgaaggagtgatgaaatatattatt	2160
Db	2146	tgaatacgaatgtaacaacagtggtgtgaaatttctgaaggagtgatgaaatatattatt	2205
Oy	2161	tcaatgggcgaactttccatttcaatttcaacacttacacatatttggctcgtgaattacaact	2220
Db	2206	tcaatgggcgaactttccatttcaatttcaacacttacacatatttggctcgtgaattacaact	2265
Oy	2221	aatttccagtatattactgtttaaattacaacaacaaggaatttattgaaagaattccgt	2280
Db	2266	aatttccagtatattactgtttaaattacaacaacaaggaatttattgaaagaattccgt	2325
Oy	2281	ttatcccgccatttgtcttgaaaaagcagcgaaagaaatttttgacttgatacagct	2340
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Oy	2341	ctgcaagagcaacttgttttcccttgcttgccttggtttccacactttgaatgaattccgt	2400
Db	2386	ctgcaagagcaacttgttgttttcccttgcttgccttggtttccacactttgaatgaattccgt	2445
Oy	2401	tttagtcaagagaagactctcttggagcaactcttatgaatacctgaatcttcttttaattgc	2460
Db	2446	tttagtcaagagaagactctcttggagcaactcttatgaatacctgaatcttcttttaattgc	2505
Oy	2461	atgaagtgattgatacgaagcaatgatatgggttatttctccctcaactggtgaatact	2520

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Db      2506 atggaagtgtatgatcatcattagacaaatgatgtgc-ttatttcctctaactgtttgaata- 2563
Qy      2521 ctttgtaacctgtcgttttgcaatalatggcgaccacaagaaggggagaga 2567
        |||||||
Db      2564 ctttgtaacctgtcgttttgcaatalatggcgaccacaagaaggagagata 2610

RESULT 10
US-09-726-810-3387
; Sequence 3387, Application US/09726810
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; FILE REFERENCE: THEREFOR
; FILE REFERENCE: 1600.2016-001
; CURRENT APPLICATION NUMBER: US/09/726,810
; CURRENT FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/168,017
; PRIOR FILING DATE: 1999-11-30
; NUMBER OF SEQ ID NOS: 3398
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3387
; LENGTH: 3545
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-726-810-3387

Query Match          94.2%; Score 2517.4; DB 29; Length 3545;
Best Local Similarity 99.3%; Fred. No. 0;
Matches 2549; Conservative 0; Mismatches 16; Indels 2; Gaps 2;
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QY	601	ctgtttacagacaatttgaaagaattatccggttttcggaaactttcaagaattgacatg	660
Db	646	ctgtttacagacaatttgaaagaattatccggttttcggaaactttcaagaattgacatg	705
QY	661	ggagatggttaacttccacatgaattccacggaaagcagaaaaaatcccgacaatggt	720
Db	706	gggataggttaacttccacatgaattccacggaaagcagaaaaaatcccgacaatggt	765
QY	721	ggagcgacgttttggcagaggagcattgctgctgtctcttcgaaaaagacatgcacct	780
Db	766	ggagcgacgttttggcagaggagcattgctgctgtctcttcgaaaaagacatgcacct	825
QY	781	tggacccgtctgaaaaatacatgatgcaggtttcacggtttcaaaaatcacagaaaatgacatat	840
Db	826	tggacccgtctgaaaaatacatgatgcaggtttcacggtttcaaaaatcacagaaaatgacatat	885
QY	841	ttggcggttttcgcaagaatgtaaagaagaagtgatccgcgtgcgttttggagggaatg	900
Db	886	ttggcggttttcgcaagaatgtaaagaagaagtgatccgcgtgcgttttggagggaatg	945
QY	901	gtacaaaagctcatcaaaaattgctcctctgaagcagctgttaaatcttgcgatatgacagt	960
Db	946	gtacaaaagctcatcaaaaattgctcctctgaagcagctgtttaaatcttgcgatatgacagt	1005
QY	961	acaagaagttacttactctgaaagaagacaaaaatagaaacatttggagattattctctg	1020
Db	1006	acaagaagttacttactctgaaagaagacaaaaatagaaacatttggagattattctctg	1065
QY	1021	gttccatgctgcggcgacaacgicgacagcttttatatccaatggagggtatgaaaaaca	1080
Db	1066	gttccatgctgcggcgacaacgicgacagcttttatatccaatggagggtatgaaaaaca	1125
QY	1081	ggctgcgcgttgaagcaaaaacgicggcgagactctggaatatatgatttgcgaaagaatt	1140
Db	1126	ggctgcgcgttgaagcaaaaacgicggcgagactctggaatatatgatttgcgaaagaatt	1185
QY	1141	tgaacaatgatgaagctctggagcgtttttacaagaagtcatttcccgaattattagttaca	1200
Db	1186	tgaacaatgatgaagcgtctggagcgtttttacaagaagtcatttcccgaattattagttaca	1245
QY	1201	taccttatgcaggatagatctctgcgtgtatgagctcttgaagtccttatgttcgctggata	1260
Db	1246	taccttatgcaggatagatctctgcgtgtatgagcgtcttgaagtccttatgttcgctggata	1305
QY	1261	attttgcaaaaagatctctgtaaacccctggaatcatgtgttgcgcggagatcggtgcctat	1320
Db	1306	attttgcaaaaagatctctgtaaacccctggaatcatgtgttgcgcggagatcggtgcctat	1365
QY	1321	ccagacacctgtgttcagcttgcgcagcgtacccatttgccttgcgttgaaactctgcacgcag	1380
Db	1366	ccagacacctgtgtgttcagcttgcgcagcgtacccatttgccttgcgttgaaactctgcacgcag	1425
QY	1381	ctcaagcgcattgttagaaggtttcccccagaagctgtaatatgtgttgcctcttctgaagaata	1440
Db	1426	ctcaagcgcattgttagaaggtttcccccagaagctgtaatatgtgttgcctcttctgaagaata	1485
QY	1441	tttccaaaagaagcagatcccgagacttacaagagcgtaccccccacaaactctcagaagcgtgc	1500
Db	1486	tttccaaaagaagcagatcccgagacttacaagagcgtaccccccacaaactctcagaagcgtgc	1545
QY	1501	tccctgctgttagcgcatacgtatgtgttatgtaaaatatgaaagcaaaacttttagaggtaa	1560
Db	1546	tccctgctgttagcgcatacgtatgtgttatgtaaaatatgaaagcaaaacttttagaggtaa	1605
QY	1561	cccgaagaatgatgttgatatttttgcgttttagcctcgttaatatgaaactttcaacaactcct	1620
Db	1606	cccgaagaatgatgttgatatttttgcgttttagcctcgttaatatgaaactttcaacaactcct	1665
QY	1621	ggagtgacttttctcctcgtaattgaaacaagcgtatgcaaaaagaagctgatatctttt	1680
Db	1666	ggagtgacttttctcctcgtaattgaaacaagcgtatgcaaaaagaagctgatatctttt	1725
QY	1681	cacaaaagggaagcgtttaacaatgtgtcatcttcaaaacttlttggcgttaaatltatagtaca	1740

Dd	1726	cacaaagggaaagctgggtaacaaaggtccacccaacttctggcgtaaatatatagttaca	1785
Qy	1741	cagaatcttcaanaatcatagatltttaaigtgttttgaaggccacacatatacttta	1800
Dd	1786	cagaatcttcaanaatcatagatltttaaigtgttttgaaggccacacatatacttta	1845
Qy	1801	tcttttcttaataactcctgcgaactctcgcctgaaatccgaaactctgaaatgtactgcg	1860
Dd	1846	tcttttcttaataactcctgcgaactctcgcctgaaatccgaaactctgaaatgtactgcg	1905
Qy	1861	ttgaaacaaattttttgtgtgttgagttaaatcatatcatcttatcttatttcgggtgt	1920
Dd	1906	ttgaaacaaattttttgtgtgttgagttaaatcatatcatcttatcttatttcgggtgt	1965
Qy	1921	ttacgtttatgcagcttccctcttlaattlaaattctcgtttatataatttgaagtcct	1980
Dd	1966	ttacgtttatgcagcttccctcttlaattlaaattctcgtttatataatttgaagtcct	2025
Qy	1981	katagattctttaaatttcccttatagaaacatlaaagaanaatcatatacttaataa	2040
Dd	2026	katagattctttaaatttcccttatagaaacatlaaagaanaatcatatacttaataa	2085
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Dd	2086	taccttcagagaanaagatcccaataagatagagtttatgcttatattttcttcagc	2145
Qy	2101	tgaatacgaatgaacaacagagtggtggaattctctgaaggagtgatgaataataattat	2160
Dd	2146	tgaatacgaatgaacaacagagtggtggaattctctgaaggagtgatgaataataattat	2205
Qy	2161	tcaagtggcactttccatttaccacgttaccatatttggttcccgaggtataaact	2220
Dd	2206	tcaagtggcactttccatttaccacgttaccatatttggttcccgaggtataaact	2265
Qy	2221	aatttcagatatactgtttaatttacaacacaaaggaatttatttgaagattcgcgt	2280
Dd	2266	aatttcagatatactgtttaatttacaacacaaaggaatttatttgaagattcgcgt	2335
Qy	2281	ttatctctgcacttgccttgganaagcagcagagaagaatatttttgaacttgcatacgt	2340
Dd	2326	ttatctctgcacttgccttgganaagcagcagagaagaatatttttgaacttgcatacgt	2385
Qy	2341	ctgcagaagcacttgttttcttccttgccttggtttccctaccctttgaatcagattcgc	2400
Dd	2386	ctgcagaagcacttgttttcttccttgccttggtttccctaccctttgaatcagattcgc	2445
Qy	2401	tttagtcaagaagaagctctctggagacatctctagtaaccttgaatcttcttttaattgc	2460
Dd	2446	tttagtcaagaagaagctctctggagacatctctagtaaccttgaatcttcttttaattgc	2505
Qy	2461	atgaagtgtgaatgatcatgtgacaagtgatgtggccttatcttccctcacactgtgtatc	2520
Dd	2506	atgaagtgtgaatgatcatgtgacaagtgatgtggccttatcttccctcacactgtgtatc	2553
Qy	2521	cttggaaactgcgtgttctgcaatatgtggcagccacaaaggggagaga	2567
Dd	2564	cttggaaactgcgtgttctgcaatatgtggcagccacaaaggggagaga	2610

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RESULT 11
US-60-213-360-3302
; Sequence 3302, Application US/60213360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
; TITLE OF INVENTION: Identified Thereby
; FILE REFERENCE: GX-0014 P
; CURRENT APPLICATION NUMBER: US/60/213,360
; CURRENT FILING DATE: 2000-06-21
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Db	1982	ataccttaacgcaaaagcatccaanaataglatagggltatagtcttattttcttcag	2041
OY	2100	ctgaatacgaatgaacacacgigtgtgaaatttcctgaagggaagatgaaattattat	2159
Db	2042	ctgaatacgaatgaacacacgigtgtgaaatttcctgaagggaagatgaaattattat	2101
OY	2160	ttcaatgggcaatttccatttaccacatgacattatttggttcctgagttacaac	2219
Db	2102	ttcagtgggcaatttccatttaccacatgacattatttggttcctgagttacaac	2161
OY	2220	taatttcaatataatactgtttaaattaccacaacaaggaatttatattgaagattccg	2279
Db	2162	taatttcaatataatactgtttaaattaccacaacaaggaatttatattgaagattccg	2221
OY	2280	ttatcccgccatctgtttgaaaagcagaggaagaagaatttttgactgtataagct	2339
Db	2222	ttatcccgccatctgtttgaaaagcagaggaagaagaatttttgactgtataagct	2281
OY	2340	tctgagagacatcttgttttcccttgctccttgcttcccttaccatttgaatcagatccg	2399
Db	2282	tctgagagacatcttgttttcccttgctccttgcttcccttaccatttgaatcagatccg	2341
OY	2400	ttttatgtaaggaagaccttcttgggaccattcttaagtaacctgaaattccttttaaty	2459
Db	2342	ttttatgtaaggaagaccttcttgggaccattcttaagtaacctgaaattccttttaaty	2401
OY	2460	catgaagtggaattgatacgaagtgatgggcttatcttcctccctcactggtgaatat	2519
Db	2402	catgaagtggaattgatacgaagtgatgggcttatcttcctccctcactggtgaatat	2460
OY	2520	cctttgaacttgcgttttgcaatatgggcagccacaagaaggggagagata	2567
Db	2461	cctttgaacttgcgttttgcaatatgggcagccacaagaagggtgagagata	2507
RESULT 12			
US-60-324-185-14440			
: Sequence 14440, Application US/60324185			
: GENERAL INFORMATION:			
: APPLICANT: Morris, MacDonald			
: APPLICANT: Lal, Preeti			
: APPLICANT: Deep, Dinu			
: TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING			
: TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE			
: FILE REFERENCE: GX-0019-1 P			
: CURRENT APPLICATION NUMBER: US/60/324, 185			
: NUMBER OF FILING DATE: 2001-09-21			
: NUMBER OF SEQ ID NOS: 35862			
: SOFTWARE: PERL Program			
: SEQ ID NO 14440			
: LENGTH: 3446			
: TYPE: DNA			
: ORGANISM: Homo sapiens			
: FEATURE:			
: NAME/KEY: misc_feature			
: OTHER INFORMATION: incyte ID NO: 221299.1			
US-60-324-185-14440			

	Query Match	Similarity	91.6%	Score 2448	DB 71	Length 3446
	Best Local	Similarity	99.3%	Pred. No. 0		
	Matches 2490	Conservative	0	Mismatches	15	Indels 3; Gaps 3
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Db	2	gcgcgtgctccgcgctcgcgccccgcagccctcgatctccgctgtaattcctcgcgacgagccg	61			
YY	121	cctgcgcctcctcggagccactgttgcgcgtcgtcgcgactcgcgagctcgcgctccaccacgcgagcct	180			

Db	62	cctgcgcctccctggagacacatgttcgcgttcgcgtgcggagacttcgtctgcgccaccgcgcgcct	121
QY	181	gccacgaacccggagacagccgcgcacgcgtacagaaacctctccaggaacccggaccgcaatg	240
Db	122	gccaggaagccggagacgacgccgaagccgcgtacagaaacctctccaggaacccggaccgcaatg	181
QY	241	ggagacggagtcgttcgacatccgcgcgcgtccgaagaggggtccagaaaccttcggccatccctc	300
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QY	301	tcggccacgaagcccgagagaaatttttactactcgtgagatgtccaagaatcgggaagc	360
Db	242	tcggccacgaagcccgagagaaatttttactactcgtgagatgtccaagaatcgggaagc	301
QY	361	tcgattttcgaagaatttatcgaagatcccttaagaagccatcgaagaagaattcgaatttcgac	420
Db	302	tcgattttcgaagaatttatcgaagatcccttaagaagccatcgaagaagaattcgaatttcgac	361
QY	421	ttcaagatcctaacaataataatgcatacgaagaatttcgaagcttcagaaatttcgcagctcc	480
Db	362	ttcaagatcctaacaataataatgcatacgaagaatttcgaagcttcagaaatttcgcagctcc	421
QY	481	tcacgaacactcgttcgtactatctcgtcaacaacgaagcagaatttcgattctcacaagcatg	540
Db	422	tcacgaacactcgttcgtactatctcgtcaacaacgaagcagaatttcgattctcacaagcatg	481
QY	541	atgcttgatggagcaatcgaacagcgcgttcgaaatgcgaatggagagacactcttatataac	600
Db	482	atgcttgatggagcaatcgaacagcgcgttcgaaatgcgaatggagagacactcttatataac	541
QY	601	ctgttcacagacactcgaagaaattacccgtcttccttcgaaacactctcaggaatttcgacatg	660
Db	542	ctgttcacagacactcgaagaaattacccgtcttccttcgaaacactctcaggaatttcgacatg	601
QY	661	gggatagccttaactatccagaatgcatacgaagaacgaaaaaaatccggacaatggt	720
Db	602	gggatagccttaactatccagaatgcatacgaagaacgaaaaaaatccggacaatggt	661
QY	721	ggagggcagcttttcgcagagagacatgtcgtcgtcgtcgtcgttcgaacacagcactgcacct	780
Db	662	ggagggcagcttttcgcagagagacatgtcgtcgtcgtcgtcgttcgaacacagcactgcacct	721
QY	781	tcgacccgtccgaataatcagatgcagcgttcacggttcacaatatccagacaatatcgaacat	840
Db	722	tcgacccgtccgaataatcagatgcagcgttcacggttcacaatatccagacaatatcgaacat	781
QY	841	ttggtgcgtcttcgaacagatcgttaaaaaagaagaggtatccgcgtcgtcttcgaggggaaatg	900
Db	782	ttggtgcgtcttcgaacagatcgttaaaaaagaagaggtatccgcgtcgtcttcgaggggaaatg	841
QY	901	gtacaaacgctacataaattgctcctcgtgacacgcgtttaaatctcgggcacatcgaacagt	960
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QY	961	acaagaatttaactcctaagaagagacaaaaataaggaaacatttcgaagattatcttcg	1020
Db	902	acaagaatttaactcctaagaagagacaaaaataaggaaacatttcgaagattatcttcg	961
QY	1021	gtccacatgcgtgagcaactgcacacgactttatatalccaaatgcgaagttaacgaaca	1080
Db	962	gtccacatgcgtgagcaactgcacacgactttatatalccaaatgcgaagttaacgaaca	1021
QY	1081	ggctgcgcgttcgagcaaaactcgggcgcgtactcctcggaatatatgattcgcgaagaagatt	1140
Db	1022	ggctgcgcgttcgagcaaaactcgggcgcgtactcctcggaatatatgattcgcgaagaagatt	1081
QY	1141	tgaaacatcgaagccttcggagagcttttccaagagctatagttcccaattatcaggtatca	1200
Db	1082	tgaaacatcgaagccttcggagagcttttccaagagctatagttcccaattatcaggtatca	1141
QY	1201	tacctaacgacgacatagatcttcgtcgttcgaagccttcgaagctcatttcgcttcggtatca	1260

Dd	1142	taactatgacgagcatgatgacttcgtctgtatgaagctcttgaagtccttatgtgcggata	1201
Oy	1261	attctgcacaaagattctgttaaacctctgtagtcaatgtgtctgtagtgcgttcctat	1320
Dd	1202	attctgcacaaagattctgttaaacctctgtagtcaatgtgtctgtagtgcgttcctat	1261
Oy	1321	ccaagacctgtgtccagctctggtccagctaccatctggtcttgtgagaatctgcagcag	1380
Dd	1262	ccaagacctgtgtccagctctggtccagctaccatctggtcttgtgagaatctgcagcag	1321
Oy	1381	ctcaagccatcttgaaggtctcccaacagctgataatgtgttgccctcttgcagaatla	1440
Dd	1322	ctcaagccatcttgaaggtctcccaacagctgataatgtgttgccctcttgcagaatla	1381
Oy	1441	ttccaagaaggaataccagagcttatacagaggtacaccccaaatctcatgaagctgc	1500
Dd	1382	ttccaagaaggaataccagagcttatacagaggtacaccccaaatctcatgaagctgc	1441
Oy	1501	tccctgcgtatgagatcaatgtatgtgttatgaaaaaatagaagcaaatcttaagatca	1560
Dd	1442	tccctgcgtatgagatcaatgtatgtgttatgaaaaaatagaagcaaatcttaagatca	1501
Oy	1561	cccaagaatgtatgtcatctttttgtgctttagccctgtgaatgaaaacttccaacatctc	1620
Dd	1502	cccaagaatgtatgtcatctttttgtgctttagccctgtgaatgaaaacttccaacatctc	1561
Oy	1621	ggagctgactttttctcctcgtaatgtaaacacagctctatggcagaagaagctgacttttt	1680
Dd	1562	ggagctgactttttctcctcgtaatgtaaacacagctctatggcagaagaagctgacttttt	1621
Oy	1681	cacaaagggaagacggttaacaatgtgtcaacttaaacctttgggttaaatatatagtca	1740
Dd	1622	cacaaagggaagacggttaacaatgtgtcaacttaaacctttgggttaaatatatagtca	1681
Oy	1741	cagaatctgttcaaaaatcaatagatttaatgtgtttgaaaaaggccacaatatatactta	1800
Dd	1682	cagaatctgttcaaaaatcaatagatttaatgtgtttgaaaaaggccacaatatatactta	1741
Oy	1801	tctttcttcaataatcctt-gcaactctctgccttgatccggaatctgaaaatgtactg	1859
Dd	1742	tctttcttcaataatccttgcctgcgaactctgccttgatccggaatctgaaaatgtactg	1801
Oy	1860	cttgaacaaaattctgttttgtgttagaggtataaatcatcaatcatcttatcttcggtg	1919
Dd	1802	cttgaacaaaattctgttttgtgttagaggtataaatcatcaatcatcttatcttcggtg	1861
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Dd	1862	tttagctttaagccagttcccttatatatatttaattcttgttatatatatttgaaagct	1921
Oy	1980	ttatagaattcttcaaatctcccttatagaaccattatagaanaatcatatataat	2039
Dd	1922	ttatagaattcttcaaatctcccttatagaaccattatagaanaatcatatataat	1981
Oy	2040	ataccttaacagcaaaagcatccaataaagtataaggttatatgtccctatcttcttcag	2099
Dd	1982	ataccttaacagcaaaagcatccaataaagtataaggttatatgtccctatcttcttcag	2041
Oy	2100	ctgaatacgaatgtaacacagatgtggaattcttcgaagggaagtatgaatatataattat	2159
Dd	2042	ctgaatacgaatgtaacacagatgtggaattcttcgaagggaagtatgaatatataattat	2101
Oy	2160	ttcagttggacattcttcattatcaacagttacatatttgttcccgaggtataac	2219
Dd	2102	ttcagttggacattcttcattatcaacagttacatatttgttcccgaggtataac	2161
Oy	2220	taatttcaatataatactgtttaaataccacaacaaggaattatatttgaagaattccg	2279
Dd	2162	taatttcaatataatactgtttaaataccacaacaaggaattatatttgaagaattccg	2221
Oy	2280	tttatctgtccatattgcttttgaaaaagcagcagaagaacgaatttttttgactgtatcagct	2339
Dd	2222	tttatctgtccatattgcttttgaaaaagcagcagaagaacgaatttttttgactgtatcagct	2281

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QY 2340 tctgcagagacatcttctgtttcttccttgccttctgtttcttcctacattgaaatcagatccg 2399
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Db 2282 tctgcagagacatcttctgtttcttccttgccttctgtttcttcctacattgaaatcagatccg 2341
QY 2400 tttagtcagagaaactctctggagccattcttagtaacctgaattctcttttaattg 2459
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Db 2342 ttctagtcagagaaactctctggagccattcttagtaacctgaattctcttttaattg 2401
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QY 2520 cctttgaactgcgtcttttgcaataatggcgacgcacaaaggggagaga 2567
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RESULT# 13
; Sequence 23662, Application US/60172360
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; FILE REFERENCE: GX-0007 P
; CURRENT APPLICATION NUMBER: US/60/172,360
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 29838
; SOFTWARE: PERL Program
; SEQ ID NO 23662
; LENGTH: 3393
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 221299.1
US-60-172-360-23662

Query Match 91.5%; Score 2446.4; DB 56; Length 3393;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 2489; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

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QY 121 cctgcgcctctcgggacccatgttcgcgtgcgcggagacttcgcgtgcgcccgcgct 180
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; GENERAL INFORMATION:

APPLICANT: Morris, MacDonald
APPLICANT: Lal, Preeti
APPLICANT: Diep, Dinh
TITLE OF INVENTION: Method for the identification of sequence polymorphisms using
TITLE OF INVENTION: Polymorphic Sequence Databases, and Single Nucleotide
TITLE OF INVENTION: Polymorphisms Identified Thereby
FILE REFERENCE: GX-0012-1 P
CURRENT APPLICATION NUMBER: US/60/278,561
CURRENT FILING DATE: 2001-03-23
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SOFTWARE: PERL Program
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LENGTH: 3446
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FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No: 221299.1
US-60-278-561-5850

Query Match 91.5%; Score 2446.4; DB 66; Length 3446;
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Db	661	gggaataagcttcaacattcccaagatccgaattccacgaaagacgaaanaaaatcccgacatg	720
OY	721	ggagagcagcttttggcagagcgacatgtgcgtgtcctcttcgaacaaagcactgtccct	780
Db	721	ggagagcagcttttggcagagcgacatgtgcgtgtcctcttcgaacaaagcactgtccct	780
OY	781	tggagccgtctgaanaataatgaatgaacgtgttcacggtttcaaatccagaacaaatgaacatat	840
Db	781	tggagccgtctgaanaataatgaatgaacgtgttcacggtttcaaatccagaacaaatgaacatat	840
OY	841	ttgggttggtcttcgacagatgtgtlaaagaagaaagtataccgcgtcgttttggaggggaaaatg	900
Db	841	ttgggttggtcttcgacagatgtgtlaaagaagaaagtataccgcgtcgttttggaggggaaaatg	900
OY	901	gtacaacaagctcatacaaaaattgtctccctcgagacagctgttaaatcttcgggcataatgaacgt	960
Db	901	gtacaacaagctcatacaaaaattgtctccctcgagacagctgttaaatcttcgggcataatgaacgt	960
OY	961	acaagaagcttcaacttaccgaagaagagacgacaaaataagaacatttgagagatttatcttcg	1020
Db	961	acaagaagcttcaacttaccgaagaagagacgacaaaataagaacatttgagagatttatcttcg	1020
OY	1021	gttccatgtgctggagcaacatcgcgcacagacttttatataccaattggaaggcttcatgaanaaca	1080
Db	1021	gttccatgtgctggagcaacatcgcgcacagacttttatataccaattggaaggcttcatgaanaaca	1080
OY	1081	ggcttggtcgttgaagcgaacaaatcgggcagtactctggaatatatgatgtgtgccaaagaattc	1140
Db	1081	ggcttggtcgttgaagcgaacaaatcgggcagtactctggaatatatgatgtgtgccaaagaattc	1140
OY	1141	tgaacatggaaggtcttggaggtttttacaagaagcattgttccaatttatagaatca	1200
Db	1141	tgaacatggaaggtcttggaggtttttacaagaagcattgttccaatttatagaatca	1200
OY	1201	tacctatgcagcagatcatgactctgctgtgatgagcgtcttgaaagctccatattgctcgagata	1260
Db	1201	tacctatgcagcagatcatgactctgctgtgatgagcgtcttgaaagctccatattgctcgagata	1260
OY	1261	attttgcaaaaagattctgttaaaccttcgaaatcagtgatgtgttcgtcgtggatgcgtgcctat	1320
Db	1261	attttgcaaaaagattctgttaaaccttcgaaatcagtgatgtgtgttcgtcgtggatgcgtgcctat	1320
OY	1321	ccagagaccttggtgcacgtctggcagacttacccatttggcttttggtagaactcgcattgcagcg	1380
Db	1321	ccagagaccttggtgcacgtctggcagacttacccatttggcttttggtagaactcgcattgcagcg	1380
OY	1381	ctcaagccatgttttgaaggtctccccaagaatgtgaatgtgttgcgctcttcgacgaatata	1440
Db	1381	ctcaagccatgttttgaaggtctccccaagaatgtgaatgtgttgcgctcttcgacgaatata	1440
OY	1441	tttccaagaagaagataccaagactttacagaggtgcatccccaacttcatgaaggtgc	1500

[illegible]

Db 1363 catgttagaaggtccccacagctgaatatglttgcccttcctgcagcaattattccaa 1422
QY 1448 agaagaataccagagacttacagagacatcaccccaaatcatgaagtgctccctgc 1507
Db 1423 agaagaataccagagacttacagagacatcaccccaaatcatgaagtgctccctgc 1482
QY 1508 tctagagcatcagttatgtgtttatgaataatgaagcaaatcttgaggttaaccagaa 1567
Db 1483 tctagagcatcagttatgtgtttatgaataatgaagcaaatcttgaggttaaccagaa 1542
QY 1568 atgattgtcatttttgccttgatgcctgaattgaactttgaacaactctcggaggtga 1627
Db 1543 atgattgtcatttttgccttgatgcctgaattgaactttgaacaactctcggaggtga 1602
QY 1628 cttttctcctcgaatttgaacaagctctatgagcaaaagagagctgtcatcttttcacaaa 1687
Db 1603 cttttctcctcgaatttgaacaagctctatgagcaaaagagagctgtcatcttttcacaaa 1662
QY 1688 ggggaagaggttaacaaatgtctactcaaacctttgggctaaattatgttacacagaaat 1747
Db 1663 ggggaagaggttaacaaatgtctactcaaacctttgggctaaattatgttacacagaaat 1722
QY 1748 gtccaaatacatagtttttaattgtgttttgaagggccacaaattatcttctttc 1807
Db 1723 gtccaaatacatagtttttaattgtgttttgaagggccacaaattatcttctttc 1782
QY 1808 ttaataatcctgcaaaatctctgacctgaatccgaaatctgaaatgtactggttggaaca 1867
Db 1783 ttaataatcctgcaaaatctctgacctgaatccgaaatctgaaatgtactggttggaaca 1842
QY 1868 aaatttggttgggtgtgtgtgaagttataaatcatatcttattctcgggtgttgctgt 1927
Db 1843 aaatttggttgggtgtgtgtgaagttataaatcatatcttattctcgggtgttgctgt 1902
QY 1928 tatgcaggttccttttatttaaatctctgtgttttattatatttgaattcctttatagt 1987
Db 1903 tatgcaggttccttttatttaaatctctgtgttttattatatttgaattcctttatagt 1962
QY 1988 tttctttaaatttctctatagaacatttaataagaataatcatatctttaaataatactta 2047
Db 1963 tttctttaaatttctctatagaacatttaataagaataatcatatctttaaataatactta 2022
QY 2048 cagcaaaagcatcccaaaataagttataggtttatgtcccttatttcttccagctgaatc 2107
Db 2023 cagcaaaagcatcccaaaataagttataggtttatgtcccttatttcttccagctgaatc 2082
QY 2108 gaattgaacacagtggtggaattctctgaagggaagtgaataattatattatcttgagtg 2167
Db 2083 gaattgaacacagtggtggaattctctgaagggaagtgaataattatattatcttgagtg 2142
QY 2168 gcaatttccatttaccactgtacattattgtgtcctgaggtatatacaactatttc 2227
Db 2143 gcaatttccatttaccactgtacattattgtgtcctgaggtatatacaactatttc 2202
QY 2228 agtatattactgtttaataatcaacaacaggaatttatgtgaagaattccggtttacct 2287
Db 2203 agtatattactgtttaataatcaacaacaggaatttatgtgaagaattccggtttacct 2262
QY 2288 gcaattgtcttgaagaagcaggaagaagaatttttgaactgtatcagctctgcaga 2347
Db 2263 gcaattgtcttgaagaagcaggaagaagaatttttgaactgtatcagctctgcaga 2322
QY 2348 gcatcttctgttcttctgttccctgttcttcccttgaacttgaacatcagatccgttttagtc 2407
Db 2323 gcatcttctgttcttctgttccctgttcttcccttgaacatcagatccgttttagtc 2382
QY 2408 aggaagaactcttggagacatctcctgaagtaacctgaattcttctttaaattgcaatgaat 2467
Db 2383 aggaagaactcttggagacatctcctgaagtaacctgaattcttctttaaattgcaatgaat 2442
QY 2468 ggaattacatagaagaagtgatgggttatttctccctcagctggtgaatacttcttga 2527
Db 2443 ggaattacatagaagaagtgatgggttatttctccctcagctggtgaatacttcttga 2500

QY 2528 ctgtcgttttgaatatgggcagccacaaaggggagaga 2567
Db 2501 ctgtcgttttgaatatgggcagccacaaaggggagaga 2540

RESULT 3

US-09-777-921A-3
; Sequence 3, Application US/09777921A
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS.
; TITLE OF INVENTION: NOCTURNAL ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS.
; FILE REFERENCE: CLO01103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 69327
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(69327)
; OTHER INFORMATION: n = A,T,C or G
US-09-777-921A-3

Query Match 42.5%; Score 1135; DB 5; Length 69327;
Best Local Similarity 98.6%; Pred. No. 4,3e-223;
Matches 1166; Conservative 0; Mismatches 15; Indels 2; Gaps 2;

QY 1385 acccaatgtaagaaggtccccaagctgaatatgtgttgcccttcctgcagcaattatttc 1444
Db 66163 acccaatgtaagaaggtccccaagctgaatatgtgttgcccttcctgcagcaattatttc 66222
QY 1445 caaagaagaataccagagacttacagagacatccccaataatcatgaagtgctccc 1504
Db 66223 caaagaagaataccagagacttacagagacatccccaataatcatgaagtgctccc 66282
QY 1505 tgcgtgagcatcagttatgtgtttatgaataatgaagcaactttgaggttaacca 1564
Db 66283 tgcgtgagcatcagttatgtgtttatgaataatgaagcaactttgaggttaacca 66342
QY 1565 gaaatgattgcatttttgcctttagccttgatgaattgaactttcaacaactctcgag 1624
Db 66343 gaaatgattgcatttttgcctttagccttgatgaattgaactttcaacaactctcgag 66402
QY 1625 tgactttctcctcgaatttgaacaagctctatggcaaaagagctgtcatctttttcaca 1684
Db 66403 tgactttctcctcgaatttgaacaagctctatggcaaaagagctgtcatctttttcaca 66462
QY 1685 aagaaggaagcgttaacaaatgtctactcaaacctttgggctaaattatataatgaacaga 1744
Db 66463 aagaaggaagcgttaacaaatgtctactcaaacctttgggctaaattatataatgaacaga 66522
QY 1745 aatgttcaaaatcatagttttaaattgtgtttgaagaagggccacaaattatattacct 1804
Db 66523 aatgttcaaaatcatagttttaaattgtgtttgaagaagggccacaaattatattacct 66582
QY 1805 tttcttaataatcctgcaaatctctgacctgaatccgaaatctgaaatgtactggtctga 1864
Db 66583 tttcttaataatcctgcaaatctctgacctgaatccgaaatctgaaatgtactggtctga 66642
QY 1865 acaaaattgtttgtgtgtgtatgaatcaatcaatcttattcttccggttggttac 1924
Db 66643 acaaaattgtttgtgtgtgtatgaatcaatcaatcttattcttccggttggttac 66702
QY 1925 gttttgcaagttccttattatatttaattctgttttatattatatttgaattgtcttata 1984
Db 66703 gttttgcaagttccttattatatttaattctgttttatattatatttgaattgtcttata 66762

QY 1985 gatttcttaattctcttataagaccattaaatagaanaatcatatcatattnaaatatacc 2044
|||||
Db 66763 gatttcttaattctcttataagaccattaaatagaanaatcatatcatattnaaatatacc 66822
QY 2045 ttaacagaaaagcaccacaataaglataggggttatagttccctatttctcttcagcgtaa 2104
|||||
Db 66823 ttacagaaaagcaccacaataaglataggggttatagttccctatttctcttcagcgtaa 66882
QY 2105 taagatagacacagtggttggaattcttgaagggaagtatgaataatataattatccag 2164
|||||
Db 66883 taagatagacacagtggttggaattcttgaagggaagtatgaataatataattatccag 66942
QY 2165 tgggcaatttccatttaccacgtacacattatttggcttcctggagttacacataat 2224
|||||
Db 66943 tgggcaatttccatttaccacgtacacattatttggcttcctggagttacacataat 67002
QY 2225 ttcaatatactgttaataataccacaacagcgcaattatattgaagaattccggttat 2284
|||||
Db 67003 ttcaatatactgttaataataccacaacagcgcaattatattgaagaattccggttat 67062
QY 2285 cctggccattcttgtaaaaagcagcaggaagaatttttgacttgtatcagctctgc 2344
|||||
Db 67063 cctggccattcttgtaaaaagcagcaggaagaatttttgacttgtatcagctctgc 67122
QY 2345 aagagcatttggcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 2404
|||||
Db 67123 aagagcatttggcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 67182
QY 2405 gtcaagagaagcattcttggacacattcttaagtaacctgaataattcttcttcaatgcaga 2464
|||||
Db 67183 gtcaagagaagcattcttggacacattcttaagtaacctgaataattcttcttcaatgcaga 67242
QY 2465 agtggatgtatcatgtgacagatgatggcttatttctccctcaactgtgtataatccttt 2524
|||||
Db 67243 agtggatgtatcatgtgacagatgatggcttatttctccctcaactgtgtataatccttt 67300
QY 2525 gaacttgctgttgcgaatcgtggcagcagcaaaaagggtgagagata 2567
|||||
Db 67301 gaacttgctgttgcgaatcgtggcagcagcaaaaagggtgagagata 67343

RESULT 4
US-09-919-002-4478
; Sequence 4478, Application US/09919002
; GENERAL INFORMATION:
; APPLICANT: Leshkowitz, Dena
; APPLICANT: Liu, Jin
; TITLE OF INVENTION: NOVEL CONFIGS OBTAINED FROM VARIOUS CDNA
; FILE REFERENCE: 20411-752CON1
; CURRENT APPLICATION NUMBER: US/09/919,002
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 09/359,922
; PRIOR FILING DATE: FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: FILING DATE: 1998-02-13
; NUMBER OF SEQ ID NOS: 13203
; SOFTWARE: FASTA/SEQ for Windows Version 3.0
; SEQ ID NO 4478
; LENGTH: 1839
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-919-002-4478

Query Match 34.9%; Score 933.4; DB 5; Length 1839;
Best Local Similarity 98.1%; Pred. No. 4,1e-182;
Matches 976; Conservative 0; Mismatches 16; Indels 3; Gaps 3;

QY 1574 ttgcatttttgccttagctagctgataatgaaacttcaacaacatcctgtgagtgactttt 1633
|||||
Db 1 ttgcatttttgccttagctagctgataatgaaacttcaacaacatcctgtgagtgactttt 60

QY 1634 ctctcgaatgaaacaagcttataggcacaagaagctgca-ttttttccaaaaaggaa 1692
|||||
Db 61 ctctcgaatgaaacaagcttataggcacaagaagctgca-ttttttccaaaaaggaa 120
QY 1693 gacgtaacaaatggcacttcaaaccttctgggtcaaatatataatgatacagaagaatgttca 1752
|||||
Db 121 gatgttaacaatggcacttcaaaccttctgggtcaaatatataatgatacagaagaatgttca 180
QY 1753 aaatcatagttttaatgtgttttgaaaaaggccacaatataacttacttcttcttaat 1812
|||||
Db 181 aaatcatagttttaatgtgttttgaaaaaggccacaatataacttacttcttcttaat 240
QY 1813 aatctcgaatctctgcccgaatccgaatctcgaatctcgaatctcgaatctcgaatctcgaat 1872
|||||
Db 241 aatctcgaatctctgcccgaatccgaatctcgaatctcgaatctcgaatctcgaatctcgaat 300
QY 1873 tgtttgtgtgtatgaatataatcattatcttcttcttcttcttcttcttcttcttcttctt 1932
|||||
Db 301 tgtttgtgtgtatgaatataatcattatcttcttcttcttcttcttcttcttcttcttctt 360
QY 1933 cagttccttataatttaattcttcttcttcttcttcttcttcttcttcttcttcttcttctt 1992
|||||
Db 361 cagttccttataatttaattcttcttcttcttcttcttcttcttcttcttcttcttcttctt 420
QY 1993 taatttcttataagacattatagaanaatcattatcattatcattatcattatcattatcatt 2052
|||||
Db 421 taatttcttataagacattatagaanaatcattatcattatcattatcattatcattatcatt 480
QY 2053 aaagcaccacaataagataaggttatagttcttcttcttcttcttcttcttcttcttcttct 2112
|||||
Db 481 aaagcaccacaataagataaggttatagttcttcttcttcttcttcttcttcttcttcttct 540
QY 2113 aacacagtggttgaatcttctgaagggaagtgaatgaatataattatcttcttcttcttct 2172
|||||
Db 541 agcacagtggttgaatcttctgaagggaagtgaatgaatataattatcttcttcttcttct 600
QY 2173 ttccatttcaacacattacattatcttcttcttcttcttcttcttcttcttcttcttcttct 2232
|||||
Db 601 ttccatttcaacacattacattatcttcttcttcttcttcttcttcttcttcttcttcttct 660
QY 2233 attactgttaaatatacacaacagaagcaattatcttgaagaatccgtttatccctgcat 2292
|||||
Db 661 attactgttaaatatacacaacagaagcaattatcttgaagaatccgtttatccctgcat 720
QY 2293 tgccttgaaaaagcagcaggaagaatcttctgaactgtatcagcttctgagagacatc 2352
|||||
Db 721 tgccttgaaaaagcagcaggaagaatcttctgaactgtatcagcttctgagagacatc 780
QY 2353 ttgtttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 2412
|||||
Db 781 ttgtttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttct 840
QY 2413 gacttcttggaacattcttgaactgaactgaactgaactgaactgaactgaactgaactgaact 2472
|||||
Db 841 gacttcttggaacattcttgaactgaactgaactgaactgaactgaactgaactgaactgaact 900
QY 2473 gatcatagagaagtgatgggttatttcttccctcaactgtgaaatcattcttgaactgtgc 2532
|||||
Db 901 gatcatagagaagtgatgggttatttcttccctcaactgtgaaatcattcttgaactgtgc 958
QY 2533 tgtttgcaatagggcagcagcacaagaagggtgagagata 2567
|||||
Db 959 tgtttgcaatagggcagcagcacaagaagggtgagagata 993

RESULT 5
US-10-158-057-38
; Sequence 38, Application US/10158057
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJ205C1

QY	736	caggagcattcgctggtgctctcccgaaacagacgctccctttggagcgcgtctcga	795
Db	638	caggagcgtgggacagggacgattctccagaaaccgcacgtcccccctggagcaagcgaag	687
QY	796	tcatgatgcaggttcacggttccaataacacagcaaaatgacataatcttggcttcac	855
Db	688	tgctatctcaggtcccatgctcccgacagcaacaatctgcatcgtgaagtgattccac	747
QY	886	agatggttaaaagaggggtatccgcgtcttgagggggaaatgtaacaagctcac	915
Db	748	agatgatctcgaagagggggagccaaagctacatctcgggggcaacggtcacaatgtccca	807
QY	916	aaatgctccctcgagacagcgtttaaattccctgggcataataacagtcagaaggttacta	975
Db	808	aaatggccctcgtcgccgcatacctaatactgcatatgacagatgaaacgctctgcg	867
QY	976	ctgaaagagcaaaaaatggaacatttgagagattatctctggttccatgtcgtgag	1035
Db	868	gtatgtatcagaagaacgctgagatccacagaaaggcttggcagagctcctctggccgag	927
QY	1036	caactgcacaaactttatatatccatgtgaggttttgaaaacagcgccgtctgtagca	1099
Db	928	ccattgcccaagtagcatctaccacaaatggaggtcttcgaagaccgaagccctggcga	987
QY	1096	aaactgggcagtaactctggaataatgatgtgtgccagaagattttgaaacatgaagct	1155
Db	988	aaacagacagtaactccgcgcatctgtaactgtgcagagagatctctgtgtaagaggtg	1047
QY	1156	tggagccttttaaaagcgtatgcttcccaatttatagtatacctaactatgacgca	1215
Db	1048	tactgctcttcaaaaggtcattaaccaccaactgtcctggggtatcaccctatgtctgca	1107
QY	1216	tagatctgtcgtgttgaagcctctcgaagctccatgtgcgtggaataatttgcgaaagatt	1279
Db	1108	tcgcagctagcgtctatagagacattgaaataaccgcgtccagcgcgtacgagtaacaa	1167
QY	1276	ctgtaaaccctgtagctataggtgtgtcctggatgcgggtgctcttaaccagaccgtgtgc	1335
Db	1168	gtgcagagcccccgggtgttctgtgtcctcctgctcgtgtgtactatccagtaactttgtgc	1227
QY	1336	agctggcagacgtaccatctgtccttggatggaactcgcgatcgaagctcaagcctgtag	1395
Db	1228	agctggcagcgtaccacactcgtccctgttgcagaccggatgtcaggaacagcttccatg	1287
QY	1396	aaggttcccaacagctgaataatgtgtgacctcttcgcagaaattatccaaagaaggaa	1455
Db	1288	aggcgacacgtgaagtaaccatgagcagcctcttcaaaagaattctcgtgactggggg	1347
QY	1456	taccaggaactttaaggggataccatacccaacttctgaagtgtctcctgtctgaagca	1515
Db	1348	cccttggtgctctacagggggcgtggccccaacttctgaagtgtatcccggtctgtgaca	1407
QY	1516	tcagttatgtgttatagaataatgaagcaaatcttaagatt	1558
Db	1408	tcagctacgtgtgtctacgaaacacctgaaatacccttggcgct	1450
RESULT 9			
US-09-312-283B-262			
: Sequence 262, Application US/09312283B			
: GENERAL INFORMATION:			
: APPLICANT: Watson, James D.			
: APPLICANT: Strachan, Lorna			
: APPLICANT: Sleeman, Matchew			
: APPLICANT: Omrust, Rene			
: APPLICANT: Murrison, James G.			
: APPLICANT: Kumble, Krishanand D.			
: TITLE OF INVENTION: Compositions and Methods for Isolated from Skin Cells			
: FILE REFERENCE: 11000.1011c2			
: CURRENT APPLICATION NUMBER: US/09/312,283B			
: CURRENT FILING DATE: 1999-05-14			

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; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Mouse
US-09-312-283B--262

```

Query Match	20.4%;	Score 545.4;	DB 5;	Length 1816;
Best Local Similarity	64.9%;	Pred. No. 2.2e-102;		
Matches 807;	Conservative 0;	Mismatches 436;	Indels 0;	Gaps 0;

OY	316	agggaaaaattttactacagggagtgtaacaaagaagggaagcggat	375
Db	216	agcggaaaaattgvcacagcaggtgcacaaaggaaccttgatgvgcaacgagccttttgaagagt	275
OY	376	ttatgaagttacctaagaagaccatgcagagaagaanaatgaaatgvcatttaagagtlttaacaa	435
Db	276	ttgtacatttacctccaagatcatgcagagaanaaactvggctggtgtlccaagagttccgaca	335
OY	436	aaaaataatgatggaanaaatgagagcttcagaaattvtccaagtcttcacagacatcgtgtc	495
Db	336	aaaagaatgatgvcagaaatctgatgtctcagagaagatcaatgcgtccctgcgvgacccgggtg	395
OY	496	tgactatttcggaacaaacagagcagagttgtatgttcaagaagcttatagtgtttgttgaca	555
Db	396	tcaagactcctcggaacacagacagcgagagaagaattcttaagaagcatgatgaabaatgcagaa	455
OY	556	tgacagatgagactggaatgaaatgagagactacttcttatttaattccgtgttaacagacatg	615
Db	456	tgaccattcagactgtgaaacagagtgagagagatcatcacactcctgcagacccctgvgagaaactcc	515
OY	616	agggaaattatccggttcttggnaaaaactttctacagaaatttaacataagggagttaagcttaata	675
Db	516	cggagatcaacctgtaactgcgaaagaacactcgcagcttcgaaatgtcgtgvgagaaatcctgcag	575
OY	676	ttccaagatgaatttcaacggaagaagcaaaaataatccggaacaaatggtgtgagcagactttgg	735
Db	576	tcccaagatgagttcatcacagvtgagagagagagcgagagatgtgtgvgagcagccctgtgtg	635
OY	736	caggagagcatgctgctggtgcgtctcttcgnaacaaagcactgcccccttttggacccgttcgaaaa	795
Db	636	caggagaggtctgvgcaggggcaggtlcttcagaaacctgcagctgcgccctcgtgcacgaactgaagg	695
OY	796	tcatgatgcagagttcatcacaggttcaaaaatcagacaanaatgaacatatgttggtgtgcttcgac	855
Db	696	tgctcatgcagagttccatgctctccgcagacaacaaatgtgcatactgtaagttgatttcacac	755
OY	856	agatggttaaaagaagagaggtataccgctcgtcttctggaggggaaatggttacaaagctcatca	915
Db	756	agatgatctcgaagaagggggagccaaatcatcactcggcgvggacaaagcatcaatgtccctca	815
OY	916	aaattgctccctgaagacagcgtttaaatctcgggcacatgaaacagatcaagaagtactta	975
Db	816	aaattgctccctgagttcggccatcaaatatcgtgcataatgacagatgaaacogcttgctgcg	875
OY	976	ctgaagaagaacaaaataagaacacattgagagattatlttcgtgtlccatcvtgctgag	1035
Db	876	gtatgtatcagagaaacgctgaagatccacaagaagcgttggtgcagactcctctgtgcggag	935
OY	1036	caactgcacagactttatatcatcgaatbgaggtatgnaaaacagcgcgtcgtgtgagca	1095
Db	936	ccattgcgccagagatgacatcatccacaatgagagttcttcgaaagcccgaaatgvcgccgtcgga	995
OY	1096	aaactggcagtaactcctggaataatagatgtgvcgaagaagaatttgaacaatgaagcgt	1155
Db	996	aaacagagacagtaactccggatgctgtagctgtgcagagagagatctcttgctaaagaggtgtg	1055
OY	1156	tgggagccttttcaaaagagctatggtlcccaatttatagatcatcaactatgtcagagca	1215
Db	1056	tagctgtccttctcaaaagagctatcatcccaacagctgtcgggagatactccctatgtctgcga	1115


```

1  APPLICANT: Grimaldi,Christopher J.
2  APPLICANT: Guaney,Austin L.
3  APPLICANT: Watanabe,Colin K.
4  APPLICANT: Wood,William I.
5  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
6  FILE REFERENCE: P3230R1C1
7  CURRENT APPLICATION NUMBER: US/10/063,502
8  CURRENT FILING DATE: 2002-05-01
9  Prior Application removed - See File Wrapper or Palm
10 NUMBER OF SEQ ID NOS: 1/0
11 SEQ ID NO 57
12 LENGTH: 3334
13 TYPE: DNA
14 ORGANISM: Homo Sapien
15 US-10-063-502-57

```

Query Match	20.3%	Score 543.8;	DB 7;	Length 3334;
Best Local Similarity	64.8%	Pred. No. 5.6e-102;		
Matches 806; Conservative	0;	Mismatches 437;	Indels 0;	Gaps 0;

QY	316	agaggaanaattttactactcgtgagatgtcaacaagaatvggaactggaatttgaagaat	375
Db	215	agcaggaanaattgttacaagctgagagataagagacttgaatgtgacgttagacttgaagaat	274
QY	376	ttatgaaggtaccttaagaagaccatgagagagaagaatgtgaattggaattagaagttagaa	435
Db	275	ttgtccattatctccaagatcatgagagaagaagcctggaagcgtggtgtttaaattttgaca	334
QY	436	aaaaataatgttgganaaataattgaggtcttcaganaaattgtccagctctctccagaacactgtgtc	495
Db	335	aaaagaatgatgagcagctgattgacgcgagagagatcatgacgtctccctgcggaacttggag	394
QY	496	tgtactattcttgacaacaacaagcagagttgattcttccaagacattgatgtatgtagaca	555
Db	395	tcaagatattctgacaacagcagcagaaaaaattctccaagacatgtgataaanaacgcgaca	454
QY	556	tgaacagtgagcttgaaatgtgagagagacacttctatttaactctgttacaagacatgt	615
Db	455	tgaaccatcgacgtggaagatgagagaaactacaacacccctccaccgccgtggaanaatccc	514
QY	616	aggaanaattacgcgttctctggaanaacattctcaagaaattgacataagagagatacttaacta	675
Db	515	ccgagatcatccctactactggaagcatccacgattccttgatgtggtgtgagatctaacg	574
QY	676	ttccagatgaattccaacggaagacgaaaaaataatccgagacaatgtgtgaggtcagctttgtg	735
Db	575	tcccgagatgtgatttacaacgtgtgagagagagacagacggtgagtgtgtgtgagaacccgttg	634
QY	736	caggaagacattcgtgtgtgtctctctccgaacaagacactgcaccttggagccgtctganaaa	795
Db	635	caggaaggtgtggtgcaggggtccggtatccaagaacctgcgaagcccccctggaagaagctacaag	694
QY	796	tcatgatgtcaggttcaacggttccaanaatcagacaanaatgaacaatattgtgtgtcttcgac	855
Db	695	tgtcatgtcaggttccatgtcctccgcgacgaacaacaatcgtcatcgttgtgtgttcaacc	754
QY	856	agatgtgtaaaagaagaggtatccgtcgtcgttvtgaggggaaatgtgtacaacgtcatcaa	915
Db	755	agatgtatctgagaaggtggtggtccaggttccaacttctcgtgcggtgcgaatgtgcatcaactcca	814
QY	916	aaattgtctctgagacagcgtgttaattctcgtgcataatgacagtaacaagaagttaactta	975
Db	815	aaattgtcccccgatacagccaatcaaatcttcatgtgcctatgtgcagatcaacaagcgttgtgtg	874
QY	976	ctgaagaagagacaaaataatgagacaattttagagattatttctgtgttccatgtcgtgag	1033
Db	875	gtagtgcacaggaagactctgagatccaagagaggtcgtgtggaaggttcccttgcaagggt	934
QY	1036	caactgtcacagacttttatataatccaatgtgaggttatgaanaaccagagctgtgcgtgtgaca	1099
Db	935	ccatcgtccaggaagaagatcatctaccatattgaggttccgtgaagacccgagatgtgcgtctcgga	994

QY	1096	aaactggtgcagtaactctcggaatatatgatgtgtgcgaagaagattttgaaacatgaagct	1155
Db	995	agacagagccagtaactcagaaatgtctgtactctgcgcagagagatctctgtgccagagaggtggtg	1054
QY	1156	tggagagcttttaacaaggagcatgttcccaattatgaatgaatcatatcactatgtacgaca	1215
Db	1055	tggcgcgctcttaacaaggatcatgttctcccaactagtgtggtcatcatccctcatgcggaca	1114
QY	1216	tagatctgtcgtatgatagctctctgaagtcctatgtctgtataatttgcanaaagatt	1275
Db	1115	tcgaactctgcagatcagaagaagctcaagaatgtcctgtgcgcagacatatgatygaaca	1174
QY	1276	ctgtaaacccctggagatcatagtgtgtctggtgagagtgctctatccagaagctgtgtgc	1335
Db	1175	gctgcgagacccgggtgttttctgtgtctctccgtgcctgtgtgcacatgtgtccagttacctgtgtcc	1234
QY	1336	agctgtgcacagctaccacattgtgctctgtgtgagaactgcacatgcagagctcaagcatgttag	1395
Db	1235	agctgtgcagatcaccctctgtgtccctcatgtcaaggcccggtgacggcgaagctctcatgt	1294
QY	1396	aagtttccccacagctgaatatgtgtgtgcctcttttcgaagaattatttccaaagaagaa	1455
Db	1295	agggtgcctccggaggtgaccatatgagaagctctcttcaaatatcctgtgcagacgggtggtg	1354
QY	1456	taccagagacttaacagagcatcacccaacttcatgaagtgtgtccctgtatgcaga	1515
Db	1355	ctcttgagctgtataaagggtgtgtcccccacacttcatgaaggtcatcccaagctgtgagca	1414
QY	1516	tcagttatgtgtgttattgaaatatgaatgaagcaaatctttagagatt	1558
Db	1415	tcagatcagttgtctacgagaacactgaatcatccctgtggtct	1457

```

RESULT 13
US-10-063-510-57
: Sequence 57, Application US/10063510
: GENERAL INFORMATION:
: APPLICANT: Eaton, Dan L.
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, Christopher J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYP
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P3230R1C1
: CURRENT APPLICATION NUMBER: US/10/063,510
: CURRENT FILING DATE: 2002-05-01
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 170
: SEQ ID NO 57
: LENGTH: 3334
: TYPE: DNA
: ORGANISM: Homo Sapien
US-10-063-510-57

```

Query Match	20.3%;	Score 543.8;	DB 7;	Length 3334;
Best Local Similarity	64.8%;	Pred. No. 5.6e-102;		
Matches 806; Conservative	0;	Mismatches 437;	Indels 0;	Gaps 0;

OY	316	agggaaaaatttttctactctaggaatgtoacaaaggttggaagcgtgatttgaagaat	375
Db	215	agcacaataattgtccaaagtcggaatcagaagccttgcgtggccctcagactttgaagaat	274
OY	376	ttatgaagtaaccttaagaagccattagaagaanaattgcatattgaattgaagtttgaaca	435
Db	275	ttgtccattatctccaaagatcatatagaagaagcgcgaagcgcgtgttttaaatattttgaca	334

QY	446	aaataatgatvggaaaaattvgagcttcagaaattgtccagcttctccagacatctggtc	495
Db	335	aaaaaagatgagtcgacatctacgcgagagatcagacgtccctcgcggnatctgggag	394
QY	446	tgacatcttcggaacaaagcagatctgtcttcacaaacatctgattgtatgvggacaa	555
Db	395	tcaagatatctcgaaacgacgacgaaaaaattctcaagagcatggtatlaaagcagca	454
QY	556	tgacagtgagctvgaaatgaaatvgagagactacttctatttaattccctgttacagacatg	615
Db	455	tgacacatctgacttgcgaacagatgtagacatcacacccctctccaccccggtgaaataatcc	514
QY	616	aggaatatcatccgttctcggaacaaactctcaagaaattgacatagvggatatagatcta	675
Db	515	ccgagatcatccctactactgtgaagcatctccacgactcttctgtgtggttgaatctca	574
QY	676	ttccagatgaaatlcacgagaaagcgaaaaaaatcccggaacatgvtgvgagcagcttttg	735
Db	575	tcccgatgtagtctcaacagtgaggtagagcgacagggagatgtgtgtagaacacttggtg	634
QY	736	cagvgagcatctgctggtgtctctctcgaaacagcactgcctctttggacccgtctga	795
Db	635	cagvgagtgvgvgcagvggcgtctacccgaacatctgcaagcctcccggaacagctcca	694
QY	796	tcatactgacagcttcaacggttccaacaaatccagaaatcgaaacatattgtgtgttcg	855
Db	695	tgctcatgtcaggtccatgtgcctcccgacgaacaaacatgagctcatctgtgtgttcac	754
QY	856	agatgvttaaagaaagagatgtaccgcgtctgtgtagvggaaatgvtacaaacgttaca	915
Db	755	agatgtatctcgaaagagagggccagctctacactctgvcgvggccaattggtcatca	814
QY	916	aaatgtgcctcgaaagcagctgttaaatctvgvggacatatgacagctcaagaaatcta	975
Db	815	aaattgcccccgaaatcagcatcaaatcatatgacctatgacatgacatcaacgcttg	874
QY	976	ctgaaagaaagcaaaaaataggaacatttgaagattattctgtgttccatvgctcgag	1033
Db	875	gtagtgaaacaaagagactctgtgagatctacagagagcctgtgacagvgctcttgc	934
QY	1036	caacgtgcacaaacttttatatcacatgtgaggtgtatgaaacaaagcctgtgctgtga	1091
Db	935	ccatctgcccaagacgacatctcaacccaatgaggtctctgaaagaccggatgvgctgc	994
QY	1096	aaactgvgcagctactctgaaatataatgattgtgccaagaaagattttgaaacatgaa	1155
Db	995	agacagcgcagctactcagaaatgtgtgactgtgcacagagagatctctgcgacag	1055
QY	1156	tgvgagcttttataaagagctatgttcccaattatagttatcatcacttatgacagga	1211
Db	1055	tgvcgctcttcaaaaagctatgttcccaacaaatgcgtggtgcatactatccctatgc	1111
QY	1216	tagactctgctgtgatgactctcttgaaatctctatcttgcgtgataattttgcgaaga	1271
Db	1115	tcgacctgtcaggtctacagagcgtgtcaagaatgtcgtgcgcagactatgacgtga	1171
QY	1276	ctgtaaaccctvgagatcatgtgtgtctgtggaatgvgggtccttatccagcacctgtgc	1331
Db	1175	gvcgagaaacccgvcgtgttctgtctctgtgctgtgtgacacacatgctcaagata	1231
QY	1336	agctvgccagctacacacatctgtcttctgttgaaatctgcacagagctccaagcatgtg	1391
Db	1235	agctvgccaagctacacccctgtgcctagtctcaagaccggatgacagvgcgcaagcct	1291
QY	1396	aaagttccccaagctgaaatagtgtgcctcttcogacgaattatltccaaagaagaa	1451
Db	1295	agvgcgtcccgaggtgtgacccaatgagcagcctcttcaaaacatactctgvcgac	1351
QY	1456	taccagagccttaacagaaatcaacaaacacatctgaagagtgctccctgtctgtatga	1511
Db	1355	cccttgvggcgtgtacagvgggtctgtgcctcccaacatctcagaaatgcatcccca	1411
QY	1516	tcagttatctgtttatbtaaaatltgaagcaaaacttttagagt	1558

[illegible]

Db 755 agatgatcagagaagagggccaggtacactctgycggggcnaatgcatcaacgtccca 814
 QY 916 aaattgctctgagacagctgttaattctggtcatatgacagtacaagaagtactta 975
 Db 815 aaattgccccgcagatcagccatcaaatctatgacctatgagcgatcaacgagccctgtg 874
 QY 976 ctgaagaagacaaaataatgacacattgagagattatctctgttccatgtgtgag 1035
 Db 875 gtatgtacacagagactctgagatctacagagaggtctgtgacaggtctctgttcagg 934
 QY 1036 caactgcacagactttatataatccaaatgaggtatgaacaacagagctgtgttagca 1095
 Db 935 ccactgccccagacagcatcaccgaatgaggtctccctgaagaccgagctgtgctgcgga 994
 QY 1096 aaactggcagactctcgagatatatgattgttgcgaagaattttgaacaatgaggtc 1155
 Db 995 agacagagccagatcagagaaatgtctgacgcgcgaagaagatccctgagcagaagagg 1054
 QY 1156 tggagacttttacaagaagctatgttcccaattatagtatcatcattatgacagca 1215
 Db 1055 tggcgactcttacaagaagctatgttcccaacatgtcggcgatcatccctatgacggca 1114
 QY 1216 taagattctgtgtatgagctcttgaagtcctaatgtgcgtgagataatttgcagaagt 1275
 Db 1115 tgcacttgcagcttcaagacgtctcaagaatgtcgtgcgcagcaactatgcagtgaca 1174
 QY 1276 ctgtaaacctgagatcatgtgtgtgtgagtcggtgtccttatccagaccctgtgtgc 1335
 Db 1175 ggcggagaccggcggtgttctgtctccgtgcgtgtgcacacatgctcagatgacgtgtgccc 1234
 QY 1336 agcttgacagacttaccatctgtgttgaagaactgcgcagagctgcacagctgttag 1395
 Db 1235 agctggcagacttaccacccctgtccctagtcagagcccgatgcagggcgcaagctctatgt 1294
 QY 1396 aaggtcccccacagctggaataatgtgtgcctcttcgacgaattatctccaagaagaa 1455
 Db 1295 aaggtcccccacagctggaataatgtgtgcctcttcgacgaattatctccaagaagaa 1354
 QY 1456 taccagagacttaccagagatcaccccaacttcaatgaggtgtccctgcgtgtgagca 1515
 Db 1355 ccttcgggctgttacaaggggctgtgcccccaacttcaatgaggtgtccctgcgtgtgagca 1414
 QY 1516 tcagttatgtgttataatgaataatgaaacatttagagt 1558
 Db 1415 tcagttatgtgttataatgaataatgaaacatttagagt 1457
 RESULT 15
 US-10-063-513-57
 : Sequence 57, Application US/10063513
 : GENERAL INFORMATION:
 : APPLICANT: Eaton, Dan L.
 : APPLICANT: Filvaroff, Ellen
 : APPLICANT: Gerritsen, Mary E.
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, Christopher J.
 : APPLICANT: Gurney, Austin L.
 : APPLICANT: Matanabe, Colin K.
 : APPLICANT: Wood, William I.
 : TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 : FILE REFERENCE: P3230R1C1
 : CURRENT APPLICATION NUMBER: US/10/063,513
 : Prior Application removed - See File Wrapper or Palm
 : NUMBER OF SEQ ID NOS: 170
 : SEQ ID NO 57
 : LENGTH: 3334
 : TYPE: DNA
 : ORGANISM: Homo Sapien
 US-10-063-513-57

Query Match 20.3%; Score 543.8; DB 7: Length 3334;
 Best Local Similarity 64.8%; Pred. No. 5,6e-102;
 Matches 806; Conservative 0; Mismatches 437; Indels 0; Gaps 0;
 QY 316 agagaanaattttactacttggagatgtlcaacaagaatgggaagcttgatttgaagaat 375
 Db 215 agcagaanaattgtacaagcttggagataagaccttggtgagcagctagtattgaagaat 274
 QY 376 ttatgaatcacttaagaacatgagaagaanaatgaaatgtgcatcttaagaattgaca 435
 Db 275 ttgtccattactccaagatcatgagaagaagctgtgaggtgtgttgaagatttggaca 334
 QY 436 aaaaatgtatgagaanaatttgaagcttccagaattgtccaggtctccacagacctgtgtc 495
 Db 335 aaaaatgtatgagaacatgtgacgcgcgagagaagatcagatcccttcggaacttggag 394
 QY 496 tgaactattctgacaacaacagcagaatgtatgttcttcaagaacatgtatgttggacaa 555
 Db 395 tcaagatattctgaacagcagcagaanaaattctcaagagcatgtgataaagaagcgaca 454
 QY 556 tgaacgtgagctgggaatgaaatgagaagaactacttataatccctgttacaagacttg 615
 Db 455 tgaacatcgaacttgaacagatggagaagactacacacccctccaccccggtggaacaacc 514
 QY 616 aggaattatccgtttcttggaaacattctacagaatttgacataggggataagcttaacta 675
 Db 515 ccgagatcacccttactatgagaagcatcccaagatctttagtgggtgagataatcaagc 574
 QY 676 ttccagaatgatttcaacgagaacgagaanaaattccgagacatgtgttgaagcagcttttg 735
 Db 575 tcccgagatgtgttacaagcttggagagagcagacgaggtatgtgttggagacacctgtgt 634
 QY 736 caggaagcattgtcgtgtgtgtctctcgtgaacaagcactgtccctttgagccgttgaaga 795
 Db 635 caggaagcttgggcagggcggtatccgaacacttgcacgccccttgagacagctcaag 694
 QY 796 tcatgtacaggttcaacgttcaaaatcagacaaatgaaatgtatgtgtgtgtgtgac 855
 Db 695 tgtcatatgacaggttccatgtcctcccgacgaacaacaaatgagcatcgtgtgtgtgtcactc 754
 QY 856 agatgttaaaagagaaggtatccgcgtcgttlttgagggggaatgtgtaacaacgtlca 915
 Db 755 agatgtatcgagaagagggggccaggtcactctgtgcgggcaatgagatcaacgttccca 814
 QY 916 aaattgtccttgagacagctgtttaaattctgycgcatatgacaacagttacaagaagtactta 975
 Db 815 aaattgtccttgagacagctgtttaaattctgycgcatatgacaacagttacaagaagtacttg 874
 QY 976 ctgaagaagacaaaataatggaacatttgaagaattatctctgttcatgagcttgag 1035
 Db 875 gtatgtacacagagactctgagatctacagagaggtctgtgacgggtctcttgcagagg 934
 QY 1036 caactgcacagactttatataatccaaatgaggtatgaacaacagagctgtgttagca 1095
 Db 935 ccactggccagagcagatcatcaccgaatgaggtgtccgaagaccggatgtgcgttcagg 994
 QY 1096 aaactggcagactctctggaatatatgattgttgcgaagaagatttgaacaatgaggtc 1155
 Db 995 agacagggccagactcagagatgtgagactgtccagagagatccttgcgacagagagg 1054
 QY 1156 tggagacttttacaagaaggtatgttcccaattatagtatcatcattatgacagca 1215
 Db 1055 tggcgactcttacaagaaggtatgttcccaacatgtcggcgatcatccctatgacggca 1114
 QY 1216 taagattctgtgtatgagctcttgaagtcctaatgtgcgtgagataatttgcagaagaat 1275
 Db 1115 tgcagacttgcagcttcaagagacgtctcaagaatgtcctgtgcgcagcatatgacgttgaca 1174
 QY 1276 ctgtaaacctgagatcatgtgtgtgtgtgagtcggtgtccttatccagaccctgtgtgc 1335
 Db 1175 ggcggagaccggcggtgttctgtctcctgtgcgtgtgacacatgttccagatcactgtgtgccc 1234

Db 61 EKIFTTGVNKGDKLDFEEFMKYLKDHKKMLAFKSLDKNNDKIEASEIVQSLOTGL 120
QY 121 TISEQOAEILLIOSIDVDGTMVDMNEMWDRYFLFNPVTDEEIIIRFKHSTGIDIGDSLTI 180
Db 121 TISEQOAEILLIOSIDVDGTMVDMNEMWDRYFLFNPVTDEEIIIRFKHSTGIDIGDSLTI 180
QY 181 PDEFTDEKSSQMMRQLLAGIAGAVSRTSTAPLDRLKIIMQVHGSKSDKNNIFGGRQ 240
Db 181 PDEFTDEKSSQMMRQLLAGIAGAVSRTSTAPLDRLKIIMQVHGSKSDKNNIFGGRQ 240
QY 241 MKKEGIRSLMGNCTNVIKIPETAVKFWAYEYQKLLTEBGOKIGTFERFISGSMGA 300
Db 241 MKKEGIRSLMGNCTNVIKIPETAVKFWAYEYQKLLTEBGOKIGTFERFISGSMGA 300
QY 301 TAQFTIYPMWKTRLAVGKTQSGIYDCAKILKHESGAFYGYVNLGIIPYAGI 360
Db 301 TAQFTIYPMWKTRLAVGKTQSGIYDCAKILKHESGAFYGYVNLGIIPYAGI 360
QY 361 DLAVYELKSYLDNFADKSNVPGVWVLLGCGALSTGQGLASTPLAVRTMQAOAMLE 420
Db 361 DLAVYELKSYLDNFADKSNVPGVWVLLGCGALSTGQGLASTPLAVRTMQAOAMLE 420
QY 421 GSPOLNMWGLFRITISKEGIPGLYRGIPNPKVLPVAGISVYVENMKOTLGVTK 477
Db 421 GSPOLNMWGLFRITISKEGIPGLYRGIPNPKVLPVAGISVYVENMKOTLGVTK 477

RESULT 2
PCT-US01-04098A-1739
; Sequence 1739, Application PC/TUS0104098A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-029
; CURRENT APPLICATION NUMBER: PCT/US01/04098A
; PRIOR APPLICATION NUMBER: Not Yet Assigned
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 09/728,422
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 09/693,325
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/663,561
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/654,936
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 09/620,325
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/598,075
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 3960
; SOFTWARE: Custom
; SEQ ID NO 1739
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-04098A-1739

Query Match 99.6%; Score 2471; DB 1; Length 477;
Best Local Similarity 99.6%; Pred. No. 1.8e-213;
Matches 475; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MRLWLDFALPTAACQDAEQPTRYETLFOALDRNGDVVDIGELQGLRNLGIPLGQDAE 60
Db 1 MRLWLDFALPTAACQDAEQPTRYETLFOALDRNGDVVDIGELQGLRNLGIPLGQDAE 60
QY 61 EKIFTTGVNKGDKLDFEEFMKYLKDHKKMLAFKSLDKNNDKIEASEIVQSLOTGL 120

Db 61 EKIFTTGVNKGDKLDFEEFMKYLKDHKKMLAFKSLDKNNDKIEASEIVQSLOTGL 120
QY 121 TISEQOAEILLIOSIDVDGTMVDMNEMWDRYFLFNPVTDEEIIIRFKHSTGIDIGDSLTI 180
Db 121 TISEQOAEILLIOSIDVDGTMVDMNEMWDRYFLFNPVTDEEIIIRFKHSTGIDIGDSLTI 180
QY 181 PDEFTDEKSSQMMRQLLAGIAGAVSRTSTAPLDRLKIIMQVHGSKSDKNNIFGGRQ 240
Db 181 PDEFTDEKSSQMMRQLLAGIAGAVSRTSTAPLDRLKIIMQVHGSKSDKNNIFGGRQ 240
QY 241 MKKEGIRSLMGNCTNVIKIPETAVKFWAYEYQKLLTEBGOKIGTFERFISGSMGA 300
Db 241 MKKEGIRSLMGNCTNVIKIPETAVKFWAYEYQKLLTEBGOKIGTFERFISGSMGA 300
QY 301 TAQFTIYPMWKTRLAVGKTQSGIYDCAKILKHESGAFYGYVNLGIIPYAGI 360
Db 301 TAQFTIYPMWKTRLAVGKTQSGIYDCAKILKHESGAFYGYVNLGIIPYAGI 360
QY 361 DLAVYELKSYLDNFADKSNVPGVWVLLGCGALSTGQGLASTPLAVRTMQAOAMLE 420
Db 361 DLAVYELKSYLDNFADKSNVPGVWVLLGCGALSTGQGLASTPLAVRTMQAOAMLE 420
QY 421 GSPOLNMWGLFRITISKEGIPGLYRGIPNPKVLPVAGISVYVENMKOTLGVTK 477
Db 421 GSPOLNMWGLFRITISKEGIPGLYRGIPNPKVLPVAGISVYVENMKOTLGVTK 477

RESULT 3
US-09-777-921-4
; Sequence 4, Application US/09777921
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C1001103
; CURRENT APPLICATION NUMBER: US/09/777,921
; CURRENT FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Rabbit
US-09-777-921-4

Query Match 95.6%; Score 2373; DB 21; Length 475;
Best Local Similarity 95.2%; Pred. No. 1.3e-204;
Matches 454; Conservative 12; Mismatches 9; Indels 2; Gaps 1;
QY 1 MRLWLDFALPTAACQDAEQPTRYETLFOALDRNGDVVDIGELQGLRNLGIPLGQDAE 60
Db 1 MRLWLDFALPTAACQDAEQPTRYETLFOALDRNGDVVDIGELQGLRNLGIPLGQDAE 60
QY 61 EKIFTTGVNKGDKLDFEEFMKYLKDHKKMLAFKSLDKNNDKIEASEIVQSLOTGL 120
Db 61 EKIFTTGVNKGDKLDFEEFMKYLKDHKKMLAFKSLDKNNDKIEASEIVQSLOTGL 120
QY 121 TISEQOAEILLIOSIDVDGTMVDMNEMWDRYFLFNPVTDEEIIIRFKHSTGIDIGDSLTI 180
Db 121 TISEQOAEILLIOSIDVDGTMVDMNEMWDRYFLFNPVTDEEIIIRFKHSTGIDIGDSLTI 180
QY 181 PDEFTDEKSSQMMRQLLAGIAGAVSRTSTAPLDRLKIIMQVHGSKSDKNNIFGGRQ 240
Db 181 PDEFTDEKSSQMMRQLLAGIAGAVSRTSTAPLDRLKIIMQVHGSKSDKNNIFGGRQ 240
QY 241 MKKEGIRSLMGNCTNVIKIPETAVKFWAYEYQKLLTEBGOKIGTFERFISGSMGA 300
Db 241 MKKEGIRSLMGNCTNVIKIPETAVKFWAYEYQKLLTEBGOKIGTFERFISGSMGA 300
QY 301 TAQFTIYPMWKTRLAVGKTQSGIYDCAKILKHESGAFYGYVNLGIIPYAGI 360
Db 301 TAQFTIYPMWKTRLAVGKTQSGIYDCAKILKHESGAFYGYVNLGIIPYAGI 360

Db 299 TAOTFYPMEMKTRLAAGTGOYSGIYDCAKKILKEGFGAFYKGYVPLNLGIIPYAGI 358
QY 361 DLAVYELLSYMLDNFAKDSVNPVWLLGCGALSTCGOLASYPALVTRMQAOMLE 420
Db 359 DLAVYELLSKSHWLDNFAKDSVNPVWLLGCGALSTCGOLASYPALVTRMQAOMLE 418
QY 421 GSPOLNMVGLFRRRIISKEGIPGLRGITPNNFMKVLPAVGISYVYVENMKOTLGYTOK 477
Db 419 GADQLNMVGLFRRRIISKEGIPGLRGITPNNFMKVLPAVGISYVYVENMKOTLGYTOK 475

RESULT 4
PCT-US01-14827-10548
; Sequence 10548, Application PC/TUS0114827
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-104
; CURRENT APPLICATION NUMBER: PCT/US01/14827
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 16102
; SOFTWARE: Custom
; SEQ ID NO 10548
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (385)..(408)
; OTHER INFORMATION: MITOCHONDRIAL CARRIER PROTEIN SIGNATURE domain identified by
; OTHER INFORMATION: EMATRX, accession number PR00926F, p-value=7.750e-19, raw score
; OTHER INFORMATION: 17.75
; NAME/KEY: DOMAIN
; LOCATION: (222)..(466)
; OTHER INFORMATION: Mitochondrial carrier proteins domain identified by Pfam,
; OTHER INFORMATION: accession name mito_carr, E-value=7.2e-71, Pfam score of 245.8
PCT-US01-14827-10548

Query Match 90.5%; Score 2246; DB 1; Length 470;
Best Local Similarity 91.4%; Pred. No. 3,6e-193;
Matches 436; Conservative 2; Mismatches 3; Indels 36; Gaps 1;

QY 1 MRLWLDLPTAACODAEOPRTYETLFOALDRNGDGVVDIGLQGLRNLGIPLODAE 60
Db 30 MRLWLDLPTAACODAEOPRTYETLFOALDRNGDGVVDIGLQGLRNLGIPLODAE 89
QY 61 EKIFTTGVDNKGKLDFFEFMKYLKDHEKKMKLAFKSLDKNNNGKLEASIEVQSLQTLGI 120
Db 90 EKIFTTGVDNKGKLDFFEFMKYLKDHEKKMKLAFKSLDKNNNGKLEASIEVQSLQTLGI 149
QY 121 TISEQDAELILOSIDVGTMTVDMNEMRDYFLFNPVTDIIEIIRFKHSTGIDIGSLTI 180
Db 150 TISEQDAELILOSIDVGTMTVDMNEMRDYFLFNPVTDIIEIIRFKHSTGIDIGSLTI 209
QY 181 PPEFTEDEKSSGQWWRROLLAGIAGVSRSTAPLDRLKIMQVHGSKSDKMIIEGFPQ 240
Db 210 PPEFTEDEKSSGQWWRROLLAGIAGVSRSTAPLDRLKIMQVHGSKSDKMIIEGFPQ 269
QY 241 MVKEGGIRSLMNGNTNVIKIAETAVKFWAYEQYKKLTIEGOKIGTFERFISGMAGA 300
Db 270 MVKEGGIRSLMNGNTNVIKIAETAVKFWAYEQYKKLTIEGOKIGTFERFISGMAGA 303
QY 301 TQOTFYPMEMKTRLAAGTGOYSGIYDCAKKILKEGFGAFYKGYVPLNLGIIPYAGI 360
Db 304 TQOTFYPMEMKTRLAAGTGOYSGIYDCAKKILKEGFGAFYKGYVPLNLGIIPYAGI 353
QY 361 DLAVYELLSYMLDNFAKDSVNPVWLLGCGALSTCGOLASYPALVTRMQAOMLE 420
Db 354 DLAVYELLSYMLDNFAKDSVNPVWLLGCGALSTCGOLASYPALVTRMQAOMLE 413

QY 421 GSPOLNMVGLFRRRIISKEGIPGLRGITPNNFMKVLPAVGISYVYVENMKOTLGYTOK 477
Db 414 GSPOLNMVGLFRRRIISKEGIPGLRGITPNNFMKVLPAVGISYVYVENMKOTLGYTOK 470

RESULT 5
US-09-777-921-5
; Sequence 5, Application US/09777921
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001103
; CURRENT APPLICATION NUMBER: US/09/777,921
; CURRENT FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Human
US-09-777-921-5

Query Match 85.9%; Score 2132; DB 21; Length 410;
Best Local Similarity 99.88; Pred. No. 5.5e-183;
Matches 409; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 FALPTAACODAEOPRTYETLFOALDRNGDGVVDIGLQGLRNLGIPLODAEKEKIFTTG 67
Db 1 FALPTAACODAEOPRTYETLFOALDRNGDGVVDIGLQGLRNLGIPLODAEKEKIFTTG 60
QY 68 DVNKGKLDFFEFMKYLKDHEKKMKLAFKSLDKNNNGKLEASIEVQSLQTLGISQQA 127
Db 61 DVNKGKLDFFEFMKYLKDHEKKMKLAFKSLDKNNNGKLEASIEVQSLQTLGISQQA 120
QY 128 ELILOSIDVGTMTVDMNEMRDYFLFNPVTDIIEIIRFKHSTGIDIGSLTIIDETED 187
Db 121 ELILOSIDVGTMTVDMNEMRDYFLFNPVTDIIEIIRFKHSTGIDIGSLTIIDETED 180
QY 188 EKSGQWWRROLLAGIAGVSRSTAPLDRLKIMQVHGSKSDKMIIEGFPQWVKEGI 247
Db 181 EKSGQWWRROLLAGIAGVSRSTAPLDRLKIMQVHGSKSDKMIIEGFPQWVKEGI 240
QY 248 RSLMNGNTNVIKIAETAVKFWAYEQYKKLTIEGOKIGTFERFISGMAGATATFTY 307
Db 241 RSLMNGNTNVIKIAETAVKFWAYEQYKKLTIEGOKIGTFERFISGMAGATATFTY 300
QY 308 PPEFTEDEKSSGQWWRROLLAGIAGVSRSTAPLDRLKIMQVHGSKSDKMIIEGFPQ 367
Db 301 PPEFTEDEKSSGQWWRROLLAGIAGVSRSTAPLDRLKIMQVHGSKSDKMIIEGFPQ 360
QY 368 LKSYWLDNFAKDSVNPVWLLGCGALSTCGOLASYPALVTRMQAOMLE 417
Db 361 LKSYWLDNFAKDSVNPVWLLGCGALSTCGOLASYPALVTRMQAOMLE 410

RESULT 6
US-09-777-921-6
; Sequence 6, Application US/09777921
; GENERAL INFORMATION:
; APPLICANT: MERKULOV et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001103
; CURRENT APPLICATION NUMBER: US/09/777,921
; CURRENT FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 342

TYPE: PRT
ORGANISM: Human
US-09-777-921-6

Query Match 71.8%; Score 1781; DB 21; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.3e-151;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 FQALDRNGDGVVDIGELQGLRNLTGIPLGDAEKKFTTGDNKDKDLDFEEMKYLKDH 87
D 1 FQALDRNGDGVVDIGELQGLRNLTGIPLGDAEKKFTTGDNKDKDLDFEEMKYLKDH 60
QY 88 EKKMKLAFSLDKNDGKIEASEIVSLQTLGLTISEQAEILLQSIDVDGTMVDMNEM 147
D 61 EKKMKLAFSLDKNDGKIEASEIVSLQTLGLTISEQAEILLQSIDVDGTMVDMNEM 120
QY 148 RDYLFNVPTDIEETIRFWKHSTGIDGSLTIPDEFTEDEKKSQOMWROLLAGIAGAV 207
D 121 RDYLFNVPTDIEETIRFWKHSTGIDGSLTIPDEFTEDEKKSQOMWROLLAGIAGAV 180
QY 208 SRTSTAPDLRLKIMQVHGSKSDKMNIFGFRQWYKEGIRSLMRNGNTNVIKIAPEYAV 267
D 181 SRTSTAPDLRLKIMQVHGSKSDKMNIFGFRQWYKEGIRSLMRNGNTNVIKIAPEYAV 240
QY 268 KFWAYEYQKLLTEEGOKIGTFERFISGSMAGATQFTIYPMYVWKTRLAVGKTGYSGI 327
D 241 KFWAYEYQKLLTEEGOKIGTFERFISGSMAGATQFTIYPMYVWKTRLAVGKTGYSGI 300
QY 328 YDCAKTKLKHGIGAFYKGYVNLGITIPYAGIDLAVYELK 369
D 301 YDCAKTKLKHGIGAFYKGYVNLGITIPYAGIDLAVYELK 342

RESULT 7
PCT-US01-21148-6
Sequence 6, Application PC/TUS0121148
GENERAL INFORMATION:
APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO00723PCT
CURRENT APPLICATION NUMBER: PCT/US01/21148
CURRENT FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 60/216,340
PRIOR FILING DATE: 2000-07-05
PRIOR APPLICATION NUMBER: 09/810,673
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 300
TYPE: PRT
ORGANISM: Human
PCT-US01-21148-6

Query Match 62.9%; Score 1560; DB 1; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 DAEOPTRYETLFQALDRNGDGVVDIGELQGLRNLTGIPLGDAEKKFTTGDNKDKGLD 76
D 1 DAEOPTRYETLFQALDRNGDGVVDIGELQGLRNLTGIPLGDAEKKFTTGDNKDKGLD 60
QY 77 FEEMKYLKDHKKMKLAFAKSLDKNDGKIEASEIVSLQTLGLTISEQAEILLQSIDV 136
D 61 FEEMKYLKDHKKMKLAFAKSLDKNDGKIEASEIVSLQTLGLTISEQAEILLQSIDV 120
QY 137 DGTMTVDMNEMRDYFLNRPVVDIEETIRFWKHSTGIDGSLTIPDEFTEDEKKSQOMW 196
D 121 DGTMTVDMNEMRDYFLNRPVVDIEETIRFWKHSTGIDGSLTIPDEFTEDEKKSQOMW 180

QY 197 QLLAGGAGAVSRSTAPDLRLKIMQVHGSKSDKMNIFGFRQWYKEGIRSLMRNGT 256
D 181 QLLAGGAGAVSRSTAPDLRLKIMQVHGSKSDKMNIFGFRQWYKEGIRSLMRNGT 240
QY 257 NVIKIAPETAVKFWAYEYQKLLTEEGOKIGTFERFISGSMAGATQFTIYPMYVWKT 316
D 241 NVIKIAPETAVKFWAYEYQKLLTEEGOKIGTFERFISGSMAGATQFTIYPMYVWKT 300

RESULT 8
US-09-810-673A-6
Sequence 6, Application US/09810673A
GENERAL INFORMATION:
APPLICANT: MERKULOV, Gennady et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLO00723
CURRENT APPLICATION NUMBER: US/09/810,673A
CURRENT FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 300
TYPE: PRT
ORGANISM: Human
US-09-810-673A-6

Query Match 62.9%; Score 1560; DB 22; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 DAEOPTRYETLFQALDRNGDGVVDIGELQGLRNLTGIPLGDAEKKFTTGDNKDKGLD 76
D 1 DAEOPTRYETLFQALDRNGDGVVDIGELQGLRNLTGIPLGDAEKKFTTGDNKDKGLD 60
QY 77 FEEMKYLKDHKKMKLAFAKSLDKNDGKIEASEIVSLQTLGLTISEQAEILLQSIDV 136
D 61 FEEMKYLKDHKKMKLAFAKSLDKNDGKIEASEIVSLQTLGLTISEQAEILLQSIDV 120
QY 137 DGTMTVDMNEMRDYFLNRPVVDIEETIRFWKHSTGIDGSLTIPDEFTEDEKKSQOMW 196
D 121 DGTMTVDMNEMRDYFLNRPVVDIEETIRFWKHSTGIDGSLTIPDEFTEDEKKSQOMW 180
QY 197 QLLAGGAGAVSRSTAPDLRLKIMQVHGSKSDKMNIFGFRQWYKEGIRSLMRNGT 256
D 181 QLLAGGAGAVSRSTAPDLRLKIMQVHGSKSDKMNIFGFRQWYKEGIRSLMRNGT 240
QY 257 NVIKIAPETAVKFWAYEYQKLLTEEGOKIGTFERFISGSMAGATQFTIYPMYVWKT 316
D 241 NVIKIAPETAVKFWAYEYQKLLTEEGOKIGTFERFISGSMAGATQFTIYPMYVWKT 300

RESULT 9
PCT-US01-04926A-194
Sequence 194, Application PC/TUS0104926A
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 21272-041
CURRENT APPLICATION NUMBER: PCT/US01/04926A
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/664,641
PRIOR FILING DATE: 2000-09-19
PRIOR APPLICATION NUMBER: 09/616,807
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 09/597,707
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/577,409
PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: 09/515,126


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; PRIOR APPLICATION NUMBER: US 60/091,626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,628
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,646
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,673
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/091,978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/091,982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/092,182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: US 60/092,472
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: US 60/093,339
; PRIOR FILING DATE: 1998-07-20
; PRIOR APPLICATION NUMBER: US 60/094,651
; PRIOR FILING DATE: 1998-07-30

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Query Match      60.5%; Score 1501; DB 21; Length 469;
Best Local Similarity 65.8%; Pred. No. 5,8e-126;
Matches 275; Conservative 71; Mismatches 72; Indels 0; Gaps 0;

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QY 60 EKKFTGGVNDGKIDFEFEFKYLLDKHKKKAKLAFKSDKNDGKIESEYISQITG 119
DB 52 KKKIVAGKRDLDGGLDFEEFVHYLDHKKKLLVKKIKDKKDRIDAOEIMQSLRDIG 111
QY 120 LKISEQOALILQSIDVDGTMVDMNEMRDFLEFNVDIEETIRFMKSTGIDIGSLT 179
DB 112 VKISEQAKILKSMKKNKTMTIDNEMRDYHLHVEVPELITLTKSTIFDVENLT 171
QY 180 IPDEFTEDKSKGQWVRLLAGIAGAVSRTSTAPLDRUKIMQVHGSKSDKNNIFGFR 239
DB 172 VDFEVEVERQGTGMWRHLVAGGAGAVSRTCTAPLDRUKVLMQVHASSNNMGIVGFT 231
QY 240 ONVKEGGISLRNGNTNYIKIAPETAVKEMVAYEQYKKILTEGCKIGTFEERISSMG 299
DB 232 QMIREGGASLWRNGINVLKTAPEISATKFMAYEQIKRLVGSQETRLRHERVAGSLAG 291
QY 300 ATAQTFIYMEYKTRLAVGKTGYSGIYDCAKKILHGBLAFYKGYVNLGIPYAG 359
DB 292 ALAQSSIVMEYKTRMALKRTGYSGMLDCARRILARBGVAFAFYGYVNMGIIPYAG 351
QY 360 IDLAVYELIKSTWLDNFAKDSVNPVGVVLLGCGALSTGQGLASYPALVTRMQAAML 419
DB 352 IDLAVYELIKNMVLDHYAVNSADPGVFLVLLAGTMSSTGQGLASYPALVTRMQAASI 411
QY 420 EGGPOLNMVGRFRIIRISKEIGLVRGIPNPMKYLPVAGISVYVYENMKOTLGVYOK 477
DB 412 EGAPEVYMSLKHILIRTEGAFGLRGLAPNPMKYLPVAVISVYVYENKLTGLVQSR 469

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RESULT 12
US-09-941-992-289

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; Sequence 289, Application US/09941992
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C1
; CURRENT APPLICATION NUMBER: US/09/941, 992
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088734
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738

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PRIOR	FILING DATE:	1998-06-10
PRIOR	APPLICATION NUMBER:	60/0887472
PRIOR	FILING DATE:	1998-06-10
PRIOR	APPLICATION NUMBER:	60/088810
PRIOR	FILING DATE:	1998-06-10
PRIOR	APPLICATION NUMBER:	60/088824
PRIOR	FILING DATE:	1998-06-10
PRIOR	APPLICATION NUMBER:	60/0888282
PRIOR	FILING DATE:	1998-06-10
PRIOR	APPLICATION NUMBER:	60/088855
PRIOR	FILING DATE:	1998-06-11
PRIOR	APPLICATION NUMBER:	60/088861
PRIOR	FILING DATE:	1998-06-11
PRIOR	APPLICATION NUMBER:	60/0888767
PRIOR	FILING DATE:	1998-06-11
PRIOR	APPLICATION NUMBER:	60/0891050
PRIOR	FILING DATE:	1998-06-12
PRIOR	APPLICATION NUMBER:	60/089440
PRIOR	FILING DATE:	1998-06-16
PRIOR	APPLICATION NUMBER:	60/089512
PRIOR	FILING DATE:	1998-06-16
PRIOR	APPLICATION NUMBER:	60/089514
PRIOR	FILING DATE:	1998-06-16
PRIOR	APPLICATION NUMBER:	60/0895232
PRIOR	FILING DATE:	1998-06-17
PRIOR	APPLICATION NUMBER:	60/089538
PRIOR	FILING DATE:	1998-06-17
PRIOR	APPLICATION NUMBER:	60/089598
PRIOR	FILING DATE:	1998-06-17
PRIOR	APPLICATION NUMBER:	60/089599
PRIOR	FILING DATE:	1998-06-17
PRIOR	APPLICATION NUMBER:	60/089600
PRIOR	FILING DATE:	1998-06-17
PRIOR	APPLICATION NUMBER:	60/0896533
PRIOR	FILING DATE:	1998-06-17
PRIOR	APPLICATION NUMBER:	60/0896747
PRIOR	FILING DATE:	1998-06-19
PRIOR	APPLICATION NUMBER:	60/089948
PRIOR	FILING DATE:	1998-06-19
PRIOR	APPLICATION NUMBER:	60/0899525
PRIOR	FILING DATE:	1998-06-19
PRIOR	APPLICATION NUMBER:	60/0902466
PRIOR	FILING DATE:	1998-06-22
PRIOR	APPLICATION NUMBER:	60/0902552
PRIOR	FILING DATE:	1998-06-22
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PRIOR	FILING DATE:	1998-06-22
PRIOR	APPLICATION NUMBER:	60/090349
PRIOR	FILING DATE:	1998-06-23
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PRIOR	FILING DATE:	1998-06-23
PRIOR	APPLICATION NUMBER:	60/090429
PRIOR	FILING DATE:	1998-06-24
PRIOR	APPLICATION NUMBER:	60/0904311
PRIOR	FILING DATE:	1998-06-24
PRIOR	APPLICATION NUMBER:	60/0904355
PRIOR	FILING DATE:	1998-06-24
PRIOR	APPLICATION NUMBER:	60/0904444
PRIOR	FILING DATE:	1998-06-24
PRIOR	APPLICATION NUMBER:	60/090445
PRIOR	FILING DATE:	1998-06-24
PRIOR	APPLICATION NUMBER:	60/090472
PRIOR	FILING DATE:	1998-06-24
PRIOR	APPLICATION NUMBER:	60/0905355
PRIOR	FILING DATE:	1998-06-24
PRIOR	APPLICATION NUMBER:	60/090540
PRIOR	FILING DATE:	1998-06-24
PRIOR	APPLICATION NUMBER:	60/090540
PRIOR	FILING DATE:	1998-06-24

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1 PRIOR APPLICATION NUMBER: 60/090542
2 PRIOR FILING DATE: 1998-06-24
3 PRIOR APPLICATION NUMBER: 60/090557
4 PRIOR FILING DATE: 1998-06-24
5 PRIOR APPLICATION NUMBER: 60/090676
6 PRIOR FILING DATE: 1998-06-25
7 PRIOR APPLICATION NUMBER: 60/090678
8 PRIOR FILING DATE: 1998-06-25
9 PRIOR APPLICATION NUMBER: 60/090690
10 PRIOR FILING DATE: 1998-06-25
11 PRIOR APPLICATION NUMBER: 60/090694
12 PRIOR FILING DATE: 1998-06-25
13 PRIOR APPLICATION NUMBER: 60/090695
14 PRIOR FILING DATE: 1998-06-25
15 PRIOR APPLICATION NUMBER: 60/090696
16 PRIOR FILING DATE: 1998-06-25
17 PRIOR APPLICATION NUMBER: 60/090862
18 PRIOR FILING DATE: 1998-06-26
19 PRIOR APPLICATION NUMBER: 60/090863
20 PRIOR FILING DATE: 1998-06-26
21 PRIOR APPLICATION NUMBER: 60/091360
22 PRIOR FILING DATE: 1998-07-01
23 PRIOR APPLICATION NUMBER: 60/091478
24 PRIOR FILING DATE: 1998-07-02
25 PRIOR APPLICATION NUMBER: 60/091544
26 PRIOR FILING DATE: 1998-07-01
27 PRIOR APPLICATION NUMBER: 60/091519
28 PRIOR FILING DATE: 1998-07-02
29 PRIOR APPLICATION NUMBER: 60/091626
30 PRIOR FILING DATE: 1998-07-02
31 PRIOR APPLICATION NUMBER: 60/091633
32 PRIOR FILING DATE: 1998-07-02
33 PRIOR APPLICATION NUMBER: 60/091978
34 PRIOR FILING DATE: 1998-07-07
35 PRIOR APPLICATION NUMBER: 60/091982
36 PRIOR FILING DATE: 1998-07-07
37 PRIOR APPLICATION NUMBER: 60/092182
38 PRIOR FILING DATE: 1998-07-09
39 PRIOR APPLICATION NUMBER: 60/092472

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Query Match	60.5%	Score 1501	DB 23	Length 469
Best Local Similarity	65.8%	Pred. 15.8e-126		
Matches 275	Conservative 71	Mismatches 72	Indels 0	Gaps 0
QY	60	EEKITTTGDVANKDKGLDFEEFMKYLKDEHEKKMKLAFKSLDKNNDKLEASETVOSLQTLTG	119	
Db	52	KOKIIOAADKDKLDGGLDPEEFEEVHYKQDEHEKKLRLEFKITLDDKNDGRIDAOEIMOSLRDGL	111	
QY	120	LITISQOAEILLQSDVNGTMTVPMNENRDFLEFPVPIIDIEKITFPMKHSNGIDIDGSLTF	179	
Db	112	VKISQOAEKLLKSLDKDKGTMTIDNENRDKDHLHPVEPIEPIILTYMKSTLFDGENTL	171	
QY	180	IPDETFDEBEKKSQGWORQLLAGIGAVSRSTAPLDRKILIMQVHSGSKDKMINTEFGGR	239	
Db	172	VPDETFVEBQRTGMMWRHLVAGGAGAVSRCTAPLDRKILVLMQVHASRNNMGIVGGPT	231	
QY	240	QMVKEGGIRSLMRNGTGNVIAKIAPETAVKFPNAYBEQYKKLLPREGOKIGTFEKFISGSNAG	299	
Db	232	QMIREGGARSLMRNGIIVNKLIPAPSAIKFPMAYBEQIKRLVSGDQSTLRIHELVAGSLAG	291	
QY	300	ATAQTFIIPMVEVMKTRLVAVGTQGYSGIYDDAKKILKEHGLCAEFKGYVPNLLGIITPYAG	359	
Db	292	AIAGSSITPMVEVLTTRMLLRKTQYSGMLDDCARILRLAEGVAEFKGYVPNMLGIITPYAG	351	
QY	360	IDLAVYELLKSTYWLDFNFAKDSVNPGEVWLLTGGALSLSTGCGOLASTPLALVTRMQAOAML	419	
Db	352	IDLAVYETLKNAMLOHYAVNSADPEVFEVLLACGTWSSFCGCGOLASTPLALVTRMQOASII	411	
QY	420	EGSQOLNMYGIFRRIRISSEGIPLGYRGTTPNPMKVLPAVGSIVYVYEMKOTLGITQK	477	
Db	412	EGAPEVYWSLFEKHLITREGAFGLRGLPAVPMKVIAPVASTIVYVENLKITTLGVQSR	469	

RESULT 13
US-09-989-279-289
; Sequence 289, Application US/09989279
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gueney, Austin L.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC56
; CURRENT APPLICATION NUMBER: US/09/989,279
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/066770
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48	PRIOR APPLICATION NUMBER: 60/091633
49	PRIOR FILING DATE: 1998-07-02
50	PRIOR APPLICATION NUMBER: 60/091978
51	PRIOR FILING DATE: 1998-07-07
52	PRIOR APPLICATION NUMBER: 60/091982
53	PRIOR FILING DATE: 1998-07-07
54	PRIOR APPLICATION NUMBER: 60/092182
55	PRIOR FILING DATE: 1998-07-09
56	PRIOR APPLICATION NUMBER: 60/092472

[illegible]

QY 240 QWKEGGJRSILMRGSGTVIATPAETAVKPMAYOYKKLTLEEOXIGTEERFLSGMG 299

Db 232 QITRRGARGARSILMRGNGINVLATIPASAKEMAYOIKRLRSGODETLRIHERLVASGLAG 291

QY 300 ATAQTFIYPMEMYKRLRLAVGKTGOYSGIYDCAKRIILKHGIGAVKGYVNNLGIIPYAG 359

Db 292 ALAQSSTIIPMELKTRMALRRTGGYSGMLDCARRILAREGVAAARYKGYVNNLGIIPYAG 351

QY 360 IDLAVYELLKSTYLDNFKADSVNPGVWVLLCGALSTTCGLASTYPLATVTRMOAOAML 419

Db 352 IDLAVYETLLKNAWLOHYAVNSADPGVEVLLACGTSMSSFCGLASTYPLATVTRMOAASI 411

QY 420 EESSPOLNMGVFRRIISKEGIPGIRGTTPNFMKVLAVGSIYVYVNMKOTLGYNQK 477

Db 412 ECAPVYTMSSLEFKHLLRTREGARGRLGRIAPNFMKVIIPAVSISYVYVNLKLTIGVOSR 469

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US-09-989-293A-289
SEQUENCE 289, APPLICATION US/09989293A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan. L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P166
CURRENT APPLICATION NUMBER: US/09/989,293A
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609

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[illegible]

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Qy 60	EKIFFTTDDVKKDKKLPDEEFEPFKLKDKHEKKMKLAFKSLDKRNDNGKLTASEIYOSLQTG	119		
Db 52	KQIVAGDDKDLDDQGLDEEFEEVYHLLQDHEKKRLVYFRTLIDKKNDGRIDAGEIQSLRDG	111		
Qy 120	LTFSQQAELLQSLIDVDGTFVDMNEMRDFELFNPYTDIEELIRPKHSTGIDIGDSL	179		
Db 112	VKISQQAEEKLIKSDKKNGTWTIDMNEWRDYLHLHPVENPEITELLYKHKSTIPDEVENLT	171		
Qy 180	IPDETDEEKSGGQMMRRLLAGTAGVSRSTAPLDRILKIMOVHSSKSDKKNIFGFR	239		
Db 172	VPDETVEERQTGMWRRLVAGGAGAVSRCTAPLDRILVLMQVHSSKSNMGIVGGF	231		
Qy 240	QMVKEGGIRSLMRNGTNGTVIKIABETAVKFWAVEQYKRLLTBEGQKIGTFEERISGMA	299		
Db 232	QMRGARGSLMRNGTNGTVIKIABETAVKFWAVEQYKRLLTBEGQKIGTFEERISGMA	291		
Qy 300	ATAQFTIPMEVMTKRLAVGTGQYSGTLYDCAKKILKHEGLGAFYKSYVNLGIIPYAG	359		
Db 292	AIASQSIYPMVELKTRMLRFTGQYSGMLDCARRILAREGAFAFYKQYVNMGLIIPYAG	351		
Qy 360	IDLAYELLKSYWIDNFKDSDVNPQVWVLGCGALSTGQGLASYPALVTRTMQAOAM	419		
Db 352	IDLAYELLKSNMLQHTAIVNSADGVEYLLACGTMSTGQGLASYPALVTRTMQAOAS	411		
Qy 420	EGSPOLNMGVLFRRIRISKEGJPGJRGITPNFMKVLPAVGISYVVENMKOTLGVTOK	477		
Db 412	EGAEFVMTSSLFHKHLTRTEGAFGLYRGLAPFMKVLPAVGSISYVVENKLTITLGVS	469		
RESULT 15	US-09-989-721-289			
	Sequence 289, Application US/09989721			
	GENERAL INFORMATION:			
	APPLICANT: Ashkenazi, Avi J.			
	APPLICANT: Baker, Kevin P.			
	APPLICANT: Botstein, David			
	APPLICANT: Desnoyers, Luc			
	APPLICANT: Eaton, Dan L.			
	APPLICANT: Ferrara, Napoleone			
	APPLICANT: Fong, Sherman			
	APPLICANT: Gerber, Hanspeter			
	APPLICANT: Gertsen, Mary E.			
	APPLICANT: Goddard, Audrey			
	APPLICANT: Godowski, Paul J.			
	APPLICANT: Gurney, Austin L.			
	APPLICANT: Kjaavin, Ivar J.			
	APPLICANT: Napier, Mary A.			
	APPLICANT: Pan, James			
	APPLICANT: Paonli, Nicholas F.			
	APPLICANT: Roy, Margaret Ann			
	APPLICANT: Stewart, Timothy A.			
	APPLICANT: Tumas, Daniel			
	APPLICANT: Watanabe, Colin K.			
	APPLICANT: Williams, P. Mickey			
	APPLICANT: Wood, William I.			
	APPLICANT: Zhang, Zemin			
	TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic			
	TITLE OF INVENTION: Acids Encoding the Same			
	FILE REFERENCE: P2730P1C55			
	CURRENT APPLICATION NUMBER: US/09/989, 721			
	CURRENT FILING DATE: 2001-11-19			
	PRIOR APPLICATION NUMBER: 60/049787			
	PRIOR FILING DATE: 1997-06-16			
	PRIOR APPLICATION NUMBER: 60/062250			
	PRIOR FILING DATE: 1997-10-17			
	PRIOR APPLICATION NUMBER: 60/065186			
	PRIOR FILING DATE: 1997-11-12			

[illegible]

1	PRIOR FILING DATE:	1998-06-16
2	PRIOR APPLICATION NUMBER:	60/089533
3	PRIOR FILING DATE:	1998-06-17
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5	PRIOR FILING DATE:	1998-06-17
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15	PRIOR FILING DATE:	1998-06-18
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17	PRIOR FILING DATE:	1998-06-18
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20	PRIOR APPLICATION NUMBER:	60/089907

PRIOR APPLICATION NUMBER: 60/0931478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/0915444
PRIOR FILING DATE: 1998-07-01
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PRIOR APPLICATION NUMBER: 60/0924722

Query Match	60.5%;	Score 1501;	DB 23;	Length 469;
Best Local Similarity	65.8%;	Pred. No. 5.8e-126;		
Matches 275;	Conservative 71;	Mismatches 72;	Indels 0;	Gaps 0;

PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089552
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/090246
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090252
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PRIOR APPLICATION NUMBER:	60/090349
PRIOR FILING DATE:	1998-06-23
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PRIOR FILING DATE:	1998-06-23
PRIOR APPLICATION NUMBER:	60/090429
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090431
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090435
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090444
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090445
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090472
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090535
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090548

[illegible]

Search completed: August 18, 2002, 09:27:03
Job time: 657 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 18, 2002, 09:21:00 ; Search time 90.36 Seconds
(without alignments)
1245.435 Million cell updates/sec

Title: US-09-777-921A-2
2481
Perfect score: 1 MLRWLRDFAALPTAACODAEQ.....VGISVYVENMKQTIGVTQK 477
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 710927 seqs, 235927762 residues

Total number of hits satisfying chosen parameters: 710927

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PC9_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2481	100.0	477	5	US-09-777-921A-2 Sequence 2, Appl
2	2373	95.6	475	5	US-09-777-921A-4 Sequence 4, Appl
3	2373	95.6	475	5	US-09-791-537-130652 Sequence 130652,
4	2132	85.9	410	5	US-09-777-921A-5 Sequence 5, Appl
5	2132	85.9	411	5	US-09-791-537-131726 Sequence 131726,
6	2132	85.9	411	7	US-60-389-987-765 Sequence 765, App
7	1781	71.8	342	5	US-09-777-921A-6 Sequence 6, Appl
8	1501	60.5	469	5	US-09-991-150-289 Sequence 289, App
9	1501	60.5	469	6	US-10-063-510-58 Sequence 58, Appl
10	1501	60.5	469	6	US-10-063-512-58 Sequence 58, Appl
11	1501	60.5	469	6	US-10-063-513-58 Sequence 58, Appl
12	1501	60.5	469	6	US-10-063-514-58 Sequence 58, Appl
13	1501	60.5	469	6	US-10-063-515-58 Sequence 58, Appl
14	1501	60.5	469	6	US-10-063-516-58 Sequence 58, Appl
15	1501	60.5	469	6	US-10-063-517-58 Sequence 58, Appl
16	1501	60.5	469	6	US-10-063-518-58 Sequence 58, Appl
17	1501	60.5	469	6	US-10-063-519-58 Sequence 58, Appl
18	1501	60.5	469	6	US-10-063-520-58 Sequence 58, Appl
19	1501	60.5	469	6	US-10-063-521-58 Sequence 58, Appl
20	1501	60.5	469	6	US-10-063-522-58 Sequence 58, Appl
21	1501	60.5	469	6	US-10-063-523-58 Sequence 58, Appl
22	1501	60.5	469	6	US-10-063-524-58 Sequence 58, Appl
23	1501	60.5	469	6	US-10-063-525-58 Sequence 58, Appl
24	1501	60.5	469	6	US-10-063-526-58 Sequence 58, Appl
25	1501	60.5	469	6	US-10-063-527-58 Sequence 58, Appl
26	1501	60.5	469	6	US-10-063-528-58 Sequence 58, Appl

27	1501	60.5	469	6	US-10-063-529-58 Sequence 58, Appl
28	1501	60.5	469	6	US-10-063-530-58 Sequence 58, Appl
29	1501	60.5	469	6	US-10-063-532-58 Sequence 58, Appl
30	1501	60.5	469	6	US-10-063-534-58 Sequence 58, Appl
31	1501	60.5	469	6	US-10-063-536-58 Sequence 58, Appl
32	1501	60.5	469	6	US-10-063-537-58 Sequence 58, Appl
33	1501	60.5	469	6	US-10-063-538-58 Sequence 58, Appl
34	1501	60.5	469	6	US-10-063-540-58 Sequence 58, Appl
35	1501	60.5	469	6	US-10-063-541-58 Sequence 58, Appl
36	1501	60.5	469	6	US-10-063-544-58 Sequence 58, Appl
37	1501	60.5	469	6	US-10-063-546-58 Sequence 58, Appl
38	1501	60.5	469	6	US-10-063-547-58 Sequence 58, Appl
39	1501	60.5	469	6	US-10-063-548-58 Sequence 58, Appl
40	1501	60.5	469	6	US-10-063-549-58 Sequence 58, Appl
41	1501	60.5	469	6	US-10-063-550-58 Sequence 58, Appl
42	1501	60.5	469	6	US-10-063-551-58 Sequence 58, Appl
43	1501	60.5	469	6	US-10-063-553-58 Sequence 58, Appl
44	1501	60.5	469	6	US-10-063-554-58 Sequence 58, Appl
45	1501	60.5	469	6	US-10-063-555-58 Sequence 58, Appl

ALIGNMENTS

RESULT 1									
US-09-777-921A-2									
; Sequence 2, Application US/09777921A									
; GENERAL INFORMATION:									
; APPLICANT: MERKULOV et al.									
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,									
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,									
; TITLE OF INVENTION: AND USES THEREOF									
; FILE REFERENCE: C1001103									
; CURRENT APPLICATION NUMBER: US/09/777, 921A									
; CURRENT FILING DATE: 2002-02-07									
; NUMBER OF SEQ ID NOS: 126									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 2									
; LENGTH: 477									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-09-777-921A-2									
Query Match 100.0%; Score 2481; DB 5; Length 477;									
Best Local Similarity 100.0%; Pred. No. 7.8e-195;									
Matches 477; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MLRWLRDFAALPTAACODAEQPTREYETLFOALDRGSDGVNDIGELQELRNIGIPLAGDAE	60						
DB	1	MLRWLRDFAALPTAACODAEQPTREYETLFOALDRGSDGVNDIGELQELRNIGIPLAGDAE	60						
QY	61	EKIFTTGVDVKKDKLDFEFPKRYLKDKHEKKMKLAFKSLDRNNDGKIBASEIVQSLQTLGL	120						
DB	61	EKIFTTGVDVKKDKLDFEFPKRYLKDKHEKKMKLAFKSLDRNNDGKIBASEIVQSLQTLGL	120						
QY	121	TISEQQAELLQSDVDGCTVTVQVNEKRDYFLRPVVDIEIRTFKWHSGCIDGDSLTI	180						
DB	121	TISEQQAELLQSDVDGCTVTVQVNEKRDYFLRPVVDIEIRTFKWHSGCIDGDSLTI	180						
QY	181	PDEFTDEKKSQGMWRRLAGAGTAGAVSRPTAPLDRLKIMQVHSGSKDKMNTFGGFRQ	240						
DB	181	PDEFTDEKKSQGMWRRLAGAGTAGAVSRPTAPLDRLKIMQVHSGSKDKMNTFGGFRQ	240						
QY	241	MKEGGIRSLMRNGTIVIKIAPETAVKFWAYEQYKRLTIEEGOKIGTFERFISGSNAGA	300						
DB	241	MKEGGIRSLMRNGTIVIKIAPETAVKFWAYEQYKRLTIEEGOKIGTFERFISGSNAGA	300						
QY	301	TAQTFIYPMVVMKTRIAVGTGQSGIYDCAKTKIKHEGIGATKYGVPVNLGITIPAGI	360						
DB	301	TAQTFIYPMVVMKTRIAVGTGQSGIYDCAKTKIKHEGIGATKYGVPVNLGITIPAGI	360						
QY	361	DLAVYELLKSYMIDNFAKDSVNPQVNVLLCGALHSTCGQLASYPALVTRRMQAAMLE	420						

```
|||||
Db 361 DLAVVELLSYWLDFNFAKSVNPGVAVLLGCGALSTSCQOLASYPALVTRTMOAAMLE 420
QY 421 GSPOLNMVGLFRRIISKEGIPGLRGITPNNPKVLPVAVGISVYVENMKOTLGTVOK 477
Db 421 GSPOLNMVGLFRRIISKEGIPGLRGITPNNPKVLPVAVGISVYVENMKOTLGTVOK 477
```

RESULT 2

US-09-777-921A-4

; Sequence 4, Application US/09777921A

; GENERAL INFORMATION:

; APPLICANT: MERKULOV et al.

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; FILE REFERENCE: C1001103

; CURRENT APPLICATION NUMBER: US/09/777,921A

; CURRENT FILING DATE: 2002-02-07

; NUMBER OF SEQ ID NOS: 126

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 475

; TYPE: PRT

; ORGANISM: Oryctolagus cuniculus

US-09-777-921A-4

Query Match 95.6%; Score 2373; DB 5; Length 475;

Best Local Similarity 95.2%; Pred. No. 5.5e-186;

Matches 454; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

```
QY 1 MLRWLDFALPTAACODAEQPTRYETLFOALDRNGDVVDIGELGRLNGLPIGODAE 60
Db 1 MLRWLDFALPTAACODAEQPTRYETLFOALDRNGDVVDIGELGRLNGLPIGODAE 60
QY 61 EKIFTTGVDNKGKLDPEEFMKYLLKDHEKKMKLAFKSLDKNDGKIEASEIVQSLOTGL 120
Db 61 EKIFTTGVDNKGKLDPEEFMKYLLKDHEKKMKLAFKSLDKNDGKIEASEIVQSLOTGL 120
QY 121 TISEQOAEELILOSIDVDGTMVDNMENMRDYLFPNVTDEIIEIRFMKSTGIDIGSLTI 180
Db 121 TISEQOAEELILOSIDVDGTMVDNMENMRDYLFPNVTDEIIEIRFMKSTGIDIGSLTI 180
QY 181 PDETFEDEKSSQGMWROLLAGIAGAVSRTSTAPLDRLKIMQVHSGSKDNINFGFRQ 240
Db 181 PDETFEDEKSSQGMWROLLAGIAGAVSRTSTAPLDRLKIMQVHSGSKDNINFGFRQ 240
QY 241 MYKEGGSRLMNGNGTNYIKIAPETAVKFWAYEYQKLLTEEGOKIGTFPERISGMAGA 300
Db 241 MYKEGGSRLMNGNGTNYIKIAPETAVKFWAYEYQKLLTEEGOKIGTFPERISGMAGA 300
QY 301 TAQTFIYPEVWKTRILAVAGTQYSGIYDCAKKILKHGELGAFYGYVNNLGIIPYAGI 360
Db 301 TAQTFIYPEVWKTRILAVAGTQYSGIYDCAKKILKHGELGAFYGYVNNLGIIPYAGI 360
QY 361 DLAVVELLSYWLDFNFAKSVNPGVAVLLGCGALSTSCQOLASYPALVTRTMOAAMLE 420
Db 361 DLAVVELLSYWLDFNFAKSVNPGVAVLLGCGALSTSCQOLASYPALVTRTMOAAMLE 420
QY 421 GSPOLNMVGLFRRIISKEGIPGLRGITPNNPKVLPVAVGISVYVENMKOTLGTVOK 477
Db 421 GSPOLNMVGLFRRIISKEGIPGLRGITPNNPKVLPVAVGISVYVENMKOTLGTVOK 477
```

RESULT 3

US-09-791-537-130652

; Sequence 130652, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Biomomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBR

```
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: Patencin version 3.0
; SEQ ID NO 130652
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-09-791-537-130652
```

Query Match 95.6%; Score 2373; DB 5; Length 475;
Best Local Similarity 95.2%; Pred. No. 5.5e-186;
Matches 454; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

```
QY 1 MLRWLDFALPTAACODAEQPTRYETLFOALDRNGDVVDIGELGRLNGLPIGODAE 60
Db 1 MLRWLDFALPTAACODAEQPTRYETLFOALDRNGDVVDIGELGRLNGLPIGODAE 60
QY 61 EKIFTTGVDNKGKLDPEEFMKYLLKDHEKKMKLAFKSLDKNDGKIEASEIVQSLOTGL 120
Db 61 EKIFTTGVDNKGKLDPEEFMKYLLKDHEKKMKLAFKSLDKNDGKIEASEIVQSLOTGL 120
QY 121 TISEQOAEELILOSIDVDGTMVDNMENMRDYLFPNVTDEIIEIRFMKSTGIDIGSLTI 180
Db 121 TISEQOAEELILOSIDVDGTMVDNMENMRDYLFPNVTDEIIEIRFMKSTGIDIGSLTI 180
QY 181 PDETFEDEKSSQGMWROLLAGIAGAVSRTSTAPLDRLKIMQVHSGSKDNINFGFRQ 240
Db 181 PDETFEDEKSSQGMWROLLAGIAGAVSRTSTAPLDRLKIMQVHSGSKDNINFGFRQ 240
QY 241 MYKEGGSRLMNGNGTNYIKIAPETAVKFWAYEYQKLLTEEGOKIGTFPERISGMAGA 300
Db 241 MYKEGGSRLMNGNGTNYIKIAPETAVKFWAYEYQKLLTEEGOKIGTFPERISGMAGA 300
QY 301 TAQTFIYPEVWKTRILAVAGTQYSGIYDCAKKILKHGELGAFYGYVNNLGIIPYAGI 360
Db 301 TAQTFIYPEVWKTRILAVAGTQYSGIYDCAKKILKHGELGAFYGYVNNLGIIPYAGI 360
QY 361 DLAVVELLSYWLDFNFAKSVNPGVAVLLGCGALSTSCQOLASYPALVTRTMOAAMLE 420
Db 361 DLAVVELLSYWLDFNFAKSVNPGVAVLLGCGALSTSCQOLASYPALVTRTMOAAMLE 420
QY 421 GSPOLNMVGLFRRIISKEGIPGLRGITPNNPKVLPVAVGISVYVENMKOTLGTVOK 477
Db 421 GSPOLNMVGLFRRIISKEGIPGLRGITPNNPKVLPVAVGISVYVENMKOTLGTVOK 477
```

RESULT 4

US-09-777-921A-5

; Sequence 5, Application US/09777921A

; GENERAL INFORMATION:

; APPLICANT: MERKULOV et al.

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; FILE REFERENCE: C1001103

; CURRENT APPLICATION NUMBER: US/09/777,921A

; CURRENT FILING DATE: 2002-02-07

; NUMBER OF SEQ ID NOS: 126

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 410

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-777-921A-5

Query Match 85.9%; Score 2132; DB 5; Length 410;
Best Local Similarity 99.8%; Pred. No. 2.5e-166;
Matches 409; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	8	FALPFAACQADAEQPRRYETTLQALDRNDQVVDIGELQBLRNLGIPLGQAAEKIFPTTG	67
	1	FLPFAACQADAEQPRRYETTLQALDRNDQVVDIGELQBLRNLGIPLGQAAEKIFPTTG	60
Qy	68	DVNMKGKIDFEFPMKYLKDHEKKMKLAFKSLDKRNDGKIEASEIYQSLQTLGTLTSEQA	12
Dp	61	DVNMKGKIDFEFPMKYLKDHEKKMKLAFKSLDKRNDGKIEASEIYQSLQTLGTLTSEQA	12
Qy	128	ELILQSIDVDGTMVDNMENRDYELFENPVDIEELIRFMKHSSTGIDIDSLTIPDETFFD	18
Dp	121	ELILQSIDVDGTMVDNMENRDYELFENPVDIEELIRFMKHSSTGIDIDSLTIPDETFFD	18
Qy	188	EKKSQMMRQLLAGIAGAVSRTSTAPLDRLKIMQVHSGSSDKMNIFFGFRQWMBEGI	24
Dp	181	EKKSQMMRQLLAGIAGAVSRTSTAPLDRLKIMQVHSGSSDKMNIFFGFRQWMBEGI	24
Qy	248	RLSMNGNSTNYIKLAPETAFFMAVEQYKKLLTEBGGKIGFFERFISGSMGATQCFEY	30
Dp	241	RLSMNGNSTNYIKLAPETAFFMAVEQYKKLLTEBGGKIGFFERFISGSMGATQCFEY	30
Qy	308	PMEVKTTRLAVGKTQGYSGIIDCAKKILKHGBLGAFFYGYVPNLLGIIIPYAGIDLAVEL	36
Dp	301	PMEVKTTRLAVGKTQGYSGIIDCAKKILKHGBLGAFFYGYVPNLLGIIIPYAGIDLAVEL	36
Qy	368	LKSTYLDNFAFADSVNPGYVULGCGALSTGCGIATYPLAVLRTRMQQA	417
Dp	361	LKSTYLDNFAFADSVNPGYVULGCGALSTGCGIATYPLAVLRTRMQQA	410

```

RESULT      5
US-09-791-537-131726
: Sequence 131726, Application US/09791537
: GENERAL INFORMATION:
: APPLICANT: Biomimix, Inc.
: APPLICANT: Debe, Derek
: APPLICANT: Danzer, Joseph
: TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
: TITLE OF INVENTION: METHODS OF USE THEREOF
: FILE REFERENCE: 261/210
: CURRENT APPLICATION NUMBER: US/09/791,537
: CURRENT FILING DATE: 2001-02-22
: NUMBER OF SEQ ID NOS: 153055
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 131726
: LENGTH: 411
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-791-537-131726

```

Query Match	85.9%	Score 2132	DB 5	Length 411
Best Local Similarity	99.8%	Pred. No. 2.5e166		
Matches 409	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

QY	8	FALPTAACODEQCTRTRETTLLQALDRNDQVVDJGELQEGRLNIGIPLGQAAEKKIFTTG	6
Dd	1	FVLPTAACQDAQEQCTRTRETTLLQALDRNDQVVDJGELQEGRLNIGIPLGQAAEKKIFTTG	60
QY	68	DVNNDDGKLIDEEEPKKYLLKDHKKKKLAFKSLDKNNDDGKTEASEYVSQITGLTISEQA	12
Dd	61	DVNNDDGKLIDEEEPKKYLLKDHKKKKLAFKSLDKNNDDGKTEASEYVSQITGLTISEQA	120
QY	128	ELLISQIDVDGTTVDVNNEMRDYELFNPVTDIETIRKWKSTGIDIDSLLTIPDEFED	18
Dd	121	ELLISQIDVDGTTVDVNNEMRDYELFNPVTDIETIRKWKSTGIDIDSLLTIPDEFED	180
QY	188	EKKSQOMMROLLAGGACAAVSTRSTAPLDRKIMMVGKSSDKNNIFGGFRQMWKEGGI	24
Dd	181	EKKSQOMMROLLAGGACAAVSTRSTAPLDRKIMMVGKSSDKNNIFGGFRQMWKEGGI	240
QY	248	RLMWGNGTNIWIKIAPETAVKFWAEQYKLLTTEGQRTGTFERETSGSMAGATAQETIY	30

Db	241	RSWMGNGNTWIKIAPETFAVFMFAVEQKKLLTEEGQKIGIFEEFFISGSMAGTAQFFIY	300
Qy	308	PHEWVKTEPLAVGKGGVSGCYIDCAKTKILKHGCLAFKGVVPNLGIIPRAGIDLAVEL	367
Db	301	PHEWVKTKRLAVGKGGVSGIITDCAKTKILKHGCLAFKGVVPNLGIIPRAGIDLAVEL	360
Qy	368	LKSYWLDNFPARDVNPVGYVLLGCGALSTSGGLASYPPLALVTRMQAQ	417
Db	361	LKSYWLDNFPARDVNPVGYVLLGCGALSTSGGLASYPPLALVTRMQAQ	410

```

RESULT      6
US-60-389-987-765
; Sequence 765: Application US/60389987
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumltra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465P2
; CURRENT APPLICATION NUMBER: US/60/389,987
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 3025
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 765
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-389-987-765

```

Query Match	85.9%	Score 2132	DB 7	Length 411
Best Local Similarity	99.8%	Pred. No. 2.5e+166		
Matches 409	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

Qy	8	FALPFAACQADAEQPRRYETFLQALDRNGDGYVDIGELQEBGRNIGTFLGQDAEKKITTTG	67
Dd	1	FVLPPAACQADAEQPRRYETFLQALDRNGDGYVDIGELQEBGRNIGTFLGQDAEKKITTTG	60
Qy	68	DVNKDGKIDFEEPMKYLKDHKKMKLAFKSLDKNNDKIEASEIVGSLQTLGLTISEQA	127
Dd	61	DVNKDGKIDFEEPMKYLKDHKKMKLAFKSLDKNNDKIEASEIVGSLQTLGLTISEQA	120
Qy	128	ELILOSIDVDGTMVDNNEWMDYFLFNPVDIEEIRFMKHSIDIGSLJTPDEFTD	187
Dd	121	ELILOSIDVDGTMVDNNEWMDYFLFNPVDIEEIRFMKHSIDIGSLJTPDEFTD	180
Qy	188	EKKSQWMMROLLAGIGAVSRSTAPLDRLKIMQVHSGSKDKMNTFGFRRMVBEGGI	247
Dd	181	EKKSQWMMROLLAGIGAVSRSTAPLDRLKIMQVHSGSKDKMNTFGFRRMVBEGGI	240
Qy	248	RLSMRGNGNTNVIKLAPEYAVFMAYEYOYKKLLTEEGOKITFERFISGSAAGTAQFTIY	307
Dd	241	RLSMRGNGNTNVIKLAPEYAVFMAYEYOYKKLLTEEGOKITFERFISGSAAGTAQFTIY	300
Qy	308	PMEVWKTFLAVGKTGOYSIGYIDCAKKLLKHGEGICAFYKGVYPNLLGIIPYAGIDLAVYEL	367
Dd	301	PMEVWKTFLAVGKTGOYSIGYIDCAKKLLKHGEGICAFYKGVYPNLLGIIPYAGIDLAVYEL	360
Qy	368	LKSYWLNDFAKDSVNPQVYMLLGGALSNSTGOLASTPLALVPRMMAQA	417
Dd	361	LKSYWLNDFAKDSVNPQVYMLLGGALSNSTGOLASTPLALVPRMMAQA	410

```

RESULT      7
US-09-777-921A-6
; Sequence 6, Application US/09777921A
; GENERAL INFORMATION:

```

```

; APPLICANT: MERKULOV et al.
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; FILE REFERENCE: AND USES THEREOF
; FILE REFERENCE: C1001103
; CURRENT APPLICATION NUMBER: US/09/777,921A
; CURRENT FILING DATE: 2002-02-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-777-921a-6
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```

Query Match          71.8%; Score 1781; DB 5; Length 342;
Best Local Similarity 100.0%; Pred. No. 1,1e-137;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

QY 28 FQALDRNGDGVVDIGELQGLRNLTGIPLGQDAEKKIFTTGDVKNKDKLDFEEFMKYLKDH 87
DB 1 FQALDRNGDGVVDIGELQGLRNLTGIPLGQDAEKKIFTTGDVKNKDKLDFEEFMKYLKDH 60
QY 88 EKKMKLAKESLDKNDGKTEASEIYOSIQTGLTISEQDAELTLOSIDVDGTMVDMNEM 147
DB 61 EKKMKLAKESLDKNDGKTEASEIYOSIQTGLTISEQDAELTLOSIDVDGTMVDMNEM 120
QY 148 RQYLFENPTDIEETIRFKHSTGIDGSLTIPDEFTDEKSGQWMLAGGAGAV 207
DB 121 RQYLFENPTDIEETIRFKHSTGIDGSLTIPDEFTDEKSGQWMLAGGAGAV 180
QY 208 SRTSTAPLDRLKIMQVHSGSKDMKNITFGFRQWYKEGIRSLWNGNGTNVTKIAPETAV 267
DB 181 SRTSTAPLDRLKIMQVHSGSKDMKNITFGFRQWYKEGIRSLWNGNGTNVTKIAPETAV 240
QY 268 KFWALEDQYKKLLTEEGOKTGFPERISGSMAGATQTFIYPHEVAKTRILAVKGTQYSGI 327
DB 241 KFWALEDQYKKLLTEEGOKTGFPERISGSMAGATQTFIYPHEVAKTRILAVKGTQYSGI 300
QY 328 YDCAKKIKLHEGIAFYKGYVNPGLIIPYAGIDLAVVELLK 369
DB 301 YDCAKKIKLHEGIAFYKGYVNPGLIIPYAGIDLAVVELLK 342
```

```

RESULT 8
; Sequence 289, Application US/09991150
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
```

```

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C48
; CURRENT APPLICATION NUMBER: US/09/991,150
; CURRENT FILING DATE: 2001-11-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 532
; SEQ ID NO 289
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-991-150-289
```

```

Query Match          60.5%; Score 1501; DB 5; Length 469;
Best Local Similarity 65.8%; Pred. No. 1,5e-114;
Matches 275; Conservative 71; Mismatches 72; Indels 0; Gaps 0;
```

```

QY 60 EKKITTTGDVKNKDKLDFEEFMKYLKDHKKKLAFLSKLDKNDGKTEASEIYOSIQTGLG 119
DB 52 KKKIYQAGKDKLDGGLDDEEFVHYLDHKKRLVFKILDKKNDRIDAOEIMOSLRDLG 111
QY 120 LTISEQDAELTLOSIDVDGTMVDMNEMRDYLFENPTDIEETIRFKHSTGIDGSLT 179
DB 112 VTISEQDAELTLOSIDVDGTMVDMNEMRDYLFENPTDIEETIRFKHSTGIDGSLT 171
QY 180 IPDEFTDEKSGQWMLAGGAGAVSRTSTAPLDRLKIMQVHSGSKDMKNITFGFR 239
DB 172 VPDEFTVEERQGMWMLHVLAVGAGAVSRTSTAPLDRLKIMQVHSGSKDMKNITFGFR 231
QY 240 QWYKGGIRSLWNGNGTNVTKIAPETAVKFWAYEDQYKKLLTEEGOKTGFPERISGSMAG 299
DB 232 QWYKGGIRSLWNGNGTNVTKIAPETAVKFWAYEDQYKKLLTEEGOKTGFPERISGSMAG 291
QY 300 ATAOTFIPMEVAKTRILAVKGTQYSGIYDCAKKIKLHEGIAFYKGYVNPGLIIPYAG 359
DB 292 ATAOTFIPMEVAKTRILAVKGTQYSGIYDCAKKIKLHEGIAFYKGYVNPGLIIPYAG 351
QY 360 IDLAVVELLKSYWLDNFAKDSVNPGLIIPYAGIYDCAKKIKLHEGIAFYKGYVNPGLIIPYAG 419
DB 352 IDLAVVELLKSYWLDNFAKDSVNPGLIIPYAGIYDCAKKIKLHEGIAFYKGYVNPGLIIPYAG 411
QY 420 EGSFQWMLAGGAGAVSRTSTAPLDRLKIMQVHSGSKDMKNITFGFRQWYKEGIRSLW 477
DB 412 EGSFQWMLAGGAGAVSRTSTAPLDRLKIMQVHSGSKDMKNITFGFRQWYKEGIRSLW 469
```

```

RESULT 9
; Sequence 58, Application US/10063502
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,502
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 58
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-063-502-58
```

Query Match	60.5%;	Score 1501;	DB 6;	Length 469;
Best Local Similarity	65.8%;	Pred. No. 1.5e-114;		
Matches 275;	Conservative 71;	Mismatches 72;	Indels 0;	Gaps 0

Qy	60	EEFETTGDNVANKOKLDPEEFEMKXIKHKKMKKIAFSLDKNDNDKTEASEIYOSIOTLG	119
Db	52	KOKTVAGDDKDDSDLDPEEFVHTLDJHEKKRLVFLVTLDDKKNDGRIDAEIYOSIULDG	111
Qy	120	LTISEDOAEILLASIDVDGTMVDMNEMWRYFLFNPTVDEIEIIRFKSHSTGIDIGSLT	179
Db	112	VKISEQOAEKILKSMKDKNGMTIDMNMWROYHLHHPENPEILLIYKXSHSTIFDVENLT	171
Qy	180	IPDEFTEDEKSGOMWFOQLLAGTAGAVSRTSPAIDRLKIMQVHSGSKDKNIFGFR	239
Db	172	VPDEFTEEEROTGMMHNLVAGGAGAVSRTCAPDRLKVLQMVHRSNNMGIVGGFT	231
Qy	240	OMWEGGIRSLWBRNGNINVIKIAPETVAKMAVQYKILTEEGOKIGTFERRISGSMAG	299
Db	232	OMIEGGARSILWBRNGINVLKIAEESAKRMAEOLIKRLVGSQOETLRIHERLVASSLAG	291
Qy	300	ATAQTFIYMEWMTRLVAVGTGQSGIYPCAKKILKHEBGLAFKYGVNLLGIIPYAG	359
Db	292	AIKASSIYPMELVLTBRMLAKRTGQYSGMELDCARRILAREGVAIFYKYGVNMLGIIPYAG	351
Qy	360	IDLAIVELLASLYWLDNFAKDSVNPGVNVLJGCGALSTGQULASYPALAVRTMRQAOAML	419
Db	352	IDLAIVETLKNAMLOHYAVNASADPGVFLVLLACGMSSTGQLASYPALAVRTMRQOAST	411
Qy	420	EGSQOLMMWGLFRILIKKEGIFPGJIKRITTFNFKVLPAVAGISVYVENMKQITGAYOK	477
Db	412	EGABEIVMSSLFKILITEGAFGJIKRILANFMKVLPAVAGISVYVENMLKITGVOSR	469

```

RESULT 10
US-10-063-510-58
Sequence 58, Application US/10063510
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Guaney, Austin L.
APPLICANT: Matanabe, Colin K.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,510
CURRENT FILING DATE: 2002-05-01
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 58
LENGTH: 469
TYPE: PRT
ORGANISM: Homo Saplen
US-10-063-510-58

```

Query Match	60.5%;	Score 1501;	DB 6;	Length 469;
Best Local Similarity	65.8%;	Pred. No. 1.5e-114;		
Matches 275;	Conservative 71;	Mismatches 72;	Indels 0;	Gaps 0

[illegible]

Qy	180	I P E T T E D E K S G O M M R O L L A G S J A G A V S R P S T P D I O R K I M M O H S K S D P K N I E G F R	239
Db	172	V P D E T T A E O R G I M M R I L V A G G G A A S R C T P L D I K L A M M H A S R S N N K I V G G F T	231
Qy	240	O M V K E G G I R S I M R G N G I N V I K I A E T A V K F M V A E O Y K R L L T E E G O K I G T E R F I S G M A G	299
Db	232	O M R E G C A R S I M R G N G I N V L T I A P E S A I K F M A Y E Q I K R L V S D D E T I R I H E R L V A G S I A G	291
Qy	300	A T A C F I T P M E V M K T R L A V G T G T Q Y S G I Y D A K I I L K H E G A R Y K R Y V P M L G I T P Y A G	355
Db	292	A I A O S S I T P M E V L T R M A L R T G T Y S G M D C A R R I L R E G A V A A Y K K Y V P M L G I T P Y A G	351
Qy	360	I D L A Y E L L K S Y M I D N F A K D S V N G P V M V L L G C G A L S T C G O L A S Y P L A V Y T R M Q A O A M L	419
Db	352	I D L A Y E T L K N A M L O H V A V N S A D P G V F L L A C G T M S S P C G L A S Y P L A V Y T R M Q A O A S I	411
Qy	420	E G S P O L N V G L F R R I R I S E G I P G L Y R G I T T P M F M V L A V A G S I S Y V Y E N M O T L E G Y O K	477
Db	412	E G A P E V M S S L F K H I L R T E G A F A G I R G L A P M F M V I P A V S I S Y V Y E N L K T T L A G O S R	469

```

RESULT 11
US-10-063-512-58
; Sequence 58, Application US/10063512
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Collin K.
APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See file wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 58
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-512-58

```

Query Match	60.5%;	Score 1501;	DB 6;	Length 469;
Best Local Similarity	65.8%;	Pred. No. 1.5e-114;		
Matches 275;	Conservative 71;	Mismatches 72;	Indels 0;	Gaps 0

Oy	60	EKKIETTDYVKKOGKLDKEEPMKTLKHEKKMKLAFMSLDKNNQKJLEASVJLOSLOTTG	119
		::: : : : : : : : : : : : : : : : : : : :	
Db	52	KOKIYQAGDKRDODGOLDEEYVHVLQDHEKKRLRYFKLIDKKNDRGRIDADEIMOSLNDLG	111
Oy	120	LTISEQOAEIIQSIDVDGTMVTDVNMENWRDYLEFENPVTIDEEILREPKHSTGIDIGSLT	179
		: :	
Db	112	VKISQOAEKKIKSIDMKKTGMTIDMNEWRDHLHPENVEIPILLKXHSTIPDVENLT	174
Oy	180	IPDETDEKESGOMWRLLAGTAGAVSRSTPLDRIKTKMMOVHOKSPKKNIPGGR	239
		: :	
Db	172	VPDETYAEROTGMMWRHLVAGGAGASRSTPLDRIKTKLMMOVHAKSRNNKQIVGGFT	231
Oy	240	QMVKBGIRSLMRNGTNGTVHIAETLAVKFAVYDQYKRLITEGQKIGTERFISGSMAG	299
		: :	
Db	232	QMIREGARSIMRNGIIVWLKIADESATKFAVYDQIRKLVGSDQETLRIRHERLVAGSLAG	291
Oy	300	ATAQCFITPMEVMTRLAVGCTQYSGIYDQAKKILKHEGAGFYKRYVYMLGIIIPYAG	359
		: :	
Db	292	AIQOSITIPMEVLTTRLMLRKTGTISGMLDQARRILAREGVAAYKIVPMMGLIIPYAG	351
Oy	360	IDLAVYELIKSEYWLIDNFKQDSVNGVAVULLGCGALISSTFCGLASVPLATVTRMQOAML	419

```
Db 352 IDLAAYETLKNAMLOHYAVNSADPGVFLACGTMSSTCGOLASYPALVTRMQOASI 411
QY 420 EGSPOLNMGLEFRRITISKEGIPGLRGITPNNMKVLPAVGISYVYVENMKOTLGVTOK 477
Db 412 EGAPVETWSLFEKHILRTREGAFGLYRGILAPNFMKVIPAVVISYVYVENLKITLGVQSR 469
```

RESULT 12

```
US-10-063-513-58
; Sequence 58, Application US/10063513
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Eaton, Dan L.
```

```
; APPLICANT: Filvaroff, Ellen
```

```
; APPLICANT: Gerritsen, Mary E.
```

```
; APPLICANT: Goddard, Audrey
```

```
; APPLICANT: Godowski, Paul J.
```

```
; APPLICANT: Grimaldi, Christopher J.
```

```
; APPLICANT: Gurney, Austin L.
```

```
; APPLICANT: Matanabe, Colin K.
```

```
; APPLICANT: Wood, William I.
```

```
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

```
; FILE REFERENCE: P3230R1C1
```

```
; CURRENT APPLICATION NUMBER: US/10/063,513
```

```
; PRIOR APPLICATION: 2002-05-01
```

```
; PRIOR APPLICATION removed - See file wrapper or Palm
```

```
; NUMBER OF SEQ ID NOS: 170
```

```
; SEQ ID NO 58
```

```
; LENGTH: 469
```

```
; TYPE: PRP
```

```
; ORGANISM: Homo Sapien
```

```
US-10-063-513-58
```

```
Query Match 60.5%; Score 1501; DB 6; Length 469;
```

```
Best Local Similarity 65.8%; Pred. No. 1.5e-114;
```

```
Matches 275; Conservative 71; Mismatches 72; Indels 0; Gaps 0;
```

```
QY 60 EKIITGDVNVKDKLDEEFEMKYLKDEHKMKLAFKSLDKNNDKIEASEIVOSLQTLG 119
Db 52 KQIVAGDCKDLDDGLDDEEFVHYLDHDEKKLRLVFKILDKKNDGRIDAOELMOSLRLDG 111
QY 120 LTFISQOAEHLIQTSDVNGTMTVDNENRDFLEPNVDIEIITFMKHSCTIDIGDSL 179
Db 112 VKISQOAEKILKSMKDKGTMTIDNENRDFYHLHPVENIPETILYMKHSTFDGEMNLT 171
QY 180 IPDEFTEDEKSGCOWMROLLAGIGAVSRSTAPLDRKIMQYHGSKDKMNIIEGGR 239
Db 172 VPDEFTEVERQGMWRRHLVAGGAGAVSRCTAPLDRKIMQYHGSKDKMNIIEGGR 231
QY 240 QMVEKGIRSLMRNGTNYIKIAPETAVKFMAYEQYKLLTEEGOKIGTFERFISGMAG 299
Db 232 QMIRGGARSLMRNGINVLKIAPESAIKFMAEQIKRLVGSDOETLRHIEHLVAGSLAG 291
QY 300 ATAQFTFPMVEYMKRLAVGTGQYSIGYDCAKKILKEHGAGAFKGYVNNLGIITPAG 359
Db 292 AIAOSSTIPMEVLTAKRLMRLKRGYSGMLDCARRILAREGVAAFYKGYVNNLGIITPAG 351
QY 360 IDLAAYETLKNAMLOHYAVNSADPGVFLACGTMSSTCGOLASYPALVTRMQOAML 419
Db 352 IDLAAYETLKNAMLOHYAVNSADPGVFLACGTMSSTCGOLASYPALVTRMQOAML 411
QY 420 EGSPOLNMGLEFRRITISKEGIPGLRGITPNNMKVLPAVGISYVYVENMKOTLGVTOK 477
Db 412 EGAPVETWSLFEKHILRTREGAFGLYRGILAPNFMKVIPAVVISYVYVENLKITLGVQSR 469
```

RESULT 13

```
US-10-063-514-58
; Sequence 58, Application US/10063514
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Eaton, Dan L.
```

```
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Matanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

```
; FILE REFERENCE: P3230R1C1
```

```
; CURRENT APPLICATION NUMBER: US/10/063,514
```

```
; PRIOR APPLICATION: 2002-05-01
```

```
; PRIOR APPLICATION removed - See file wrapper or Palm
```

```
; NUMBER OF SEQ ID NOS: 170
```

```
; SEQ ID NO 58
```

```
; LENGTH: 469
```

```
; TYPE: PRP
```

```
; ORGANISM: Homo Sapien
```

```
US-10-063-514-58
```

```
Query Match 60.5%; Score 1501; DB 6; Length 469;
```

```
Best Local Similarity 65.8%; Pred. No. 1.5e-114;
```

```
Matches 275; Conservative 71; Mismatches 72; Indels 0; Gaps 0;
```

```
QY 60 EKIITGDVNVKDKLDEEFEMKYLKDEHKMKLAFKSLDKNNDKIEASEIVOSLQTLG 119
Db 52 KQIVAGDCKDLDDGLDDEEFVHYLDHDEKKLRLVFKILDKKNDGRIDAOELMOSLRLDG 111
QY 120 LTFISQOAEHLIQTSDVNGTMTVDNENRDFLEPNVDIEIITFMKHSCTIDIGDSL 179
Db 112 VKISQOAEKILKSMKDKGTMTIDNENRDFYHLHPVENIPETILYMKHSTFDGEMNLT 171
QY 180 IPDEFTEDEKSGCOWMROLLAGIGAVSRSTAPLDRKIMQYHGSKDKMNIIEGGR 239
Db 172 VPDEFTEVERQGMWRRHLVAGGAGAVSRCTAPLDRKIMQYHGSKDKMNIIEGGR 231
QY 240 QMVEKGIRSLMRNGTNYIKIAPETAVKFMAYEQYKLLTEEGOKIGTFERFISGMAG 299
Db 232 QMIRGGARSLMRNGINVLKIAPESAIKFMAEQIKRLVGSDOETLRHIEHLVAGSLAG 291
QY 300 ATAQFTFPMVEYMKRLAVGTGQYSIGYDCAKKILKEHGAGAFKGYVNNLGIITPAG 359
Db 292 AIAOSSTIPMEVLTAKRLMRLKRGYSGMLDCARRILAREGVAAFYKGYVNNLGIITPAG 351
QY 360 IDLAAYETLKNAMLOHYAVNSADPGVFLACGTMSSTCGOLASYPALVTRMQOAML 419
Db 352 IDLAAYETLKNAMLOHYAVNSADPGVFLACGTMSSTCGOLASYPALVTRMQOAML 411
QY 420 EGSPOLNMGLEFRRITISKEGIPGLRGITPNNMKVLPAVGISYVYVENMKOTLGVTOK 477
Db 412 EGAPVETWSLFEKHILRTREGAFGLYRGILAPNFMKVIPAVVISYVYVENLKITLGVQSR 469
```

RESULT 14

```
US-10-063-515-58
; Sequence 58, Application US/10063515
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Eaton, Dan L.
```

```
; APPLICANT: Filvaroff, Ellen
```

```
; APPLICANT: Gerritsen, Mary E.
```

```
; APPLICANT: Goddard, Audrey
```

```
; APPLICANT: Godowski, Paul J.
```

```
; APPLICANT: Grimaldi, Christopher J.
```

```
; APPLICANT: Gurney, Austin L.
```

```
; APPLICANT: Matanabe, Colin K.
```

```
; APPLICANT: Wood, William I.
```

```
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
```

```
; FILE REFERENCE: P3230R1C1
```

```
; CURRENT APPLICATION NUMBER: US/10/063,515
```

```
; CURRENT FILING DATE: 2002-05-01
```

; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 58
 ; LENGTH: 469
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-063-515-58

Query Match 60.5%; Score 1501; DB 6; Length 469;
 Best Local Similarity 65.8%; Pred. No. 1.5e-114;
 Matches 275; Conservative 71; Mismatches 72; Indels 0; Gaps 0;

```

QY 60 EEKIFTTGVNKKDKLDLFEFEFMKYLKDHEKKMKLAFKSLDKNNDKIEASEIVOSLQTLG 119
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 52 KQKIVAGDKDLDGQDLDFEEFVHYLDHKKLRLVFKILDKKNGRIDAOEIMQSLRDLG 111
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 120 LITSEQOAEILLOSIDVDGIMTVDMNEMRDYFLFNPVTDIEEIRFMKHSSTGIDIGSLT 179
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 112 VKISEQOAEKILKSMKNGMTITDMNEMRDYHLHPEVNIPEIILYWKHSSTFDVGENLT 171
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 180 IPDEFTEDEKSSGOWMROLLAGIAGAVSRSTAPLDRLKIMQVHSGSKDKNNITGGER 239
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 172 VPDEFTEERQGTMMHRLVAGGAGAVSRCTAPLDRLKVLQVHASRSNNMGIVGGFT 231
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 240 QMWKEGIRSILMRNGNTNVIKIAPEYAVKFWAYEQYKLLTEEGOKIGTFEERFTSGSMAG 299
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 232 QMIREGARSIMRNGINVLKIAPESAIKFMAYEQIKRLVSGDETLRIHERLVAGSLAG 291
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 300 ATAQFTIYPMEVKTRFLAVGKTGOYSIGYDCAKKILKHESGLGAFYKGYVPMNLGITIPYAG 359
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 292 AIAOSSIYPMEEVLKTRMALRKRTGOYSGMLDCARRILAREGVAAFYKGYVPMNLGITIPYAG 351
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 360 IDLAAYELLKSYWLDNFAPKDSVNPVNLGCGALSTCGQLASYPLALVTRMQAOAML 419
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 352 IDLAAYETTLKNAWLQHYAVNSADPGVFLLAGCTMSSTCGQLASYPLALVTRMQAOAST 411
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 420 EGSPOLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISIVYVENMKOTLGVTK 477
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 412 EGAPETVMSLFRHLTLRTGAFGLYRGLAPNFMKVIIPAVSISIVYVENLKITLGVQSR 469
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  
```

RESULT 15
 US-10-063-516-58
 ; Sequence 58, Application US/10063516
 ; GENERAL INFORMATION:
 ; APPLICANT: Baton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,516
 ; CURRENT FILING DATE: 2002-05-01
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 58
 ; LENGTH: 469
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-063-516-58

Query Match 60.5%; Score 1501; DB 6; Length 469;
 Best Local Similarity 65.8%; Pred. No. 1.5e-114;
 Matches 275; Conservative 71; Mismatches 72; Indels 0; Gaps 0;

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QY 60 EEKIFTTGVNKKDKLDLFEFEFMKYLKDHEKKMKLAFKSLDKNNDKIEASEIVOSLQTLG 119
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DB 52 KQKIVAGDKDLDGQDLDFEEFVHYLDHKKLRLVFKILDKKNGRIDAOEIMQSLRDLG 111
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 120 LITSEQOAEILLOSIDVDGIMTVDMNEMRDYFLFNPVTDIEEIRFMKHSSTGIDIGSLT 179
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 112 VKISEQOAEKILKSMKNGMTITDMNEMRDYHLHPEVNIPEIILYWKHSSTFDVGENLT 171
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QY 180 IPDEFTEDEKSSGOWMROLLAGIAGAVSRSTAPLDRLKIMQVHSGSKDKNNITGGER 239
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DB 172 VPDEFTEERQGTMMHRLVAGGAGAVSRCTAPLDRLKVLQVHASRSNNMGIVGGFT 231
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 240 QMWKEGIRSILMRNGNTNVIKIAPEYAVKFWAYEQYKLLTEEGOKIGTFEERFTSGSMAG 299
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 232 QMIREGARSIMRNGINVLKIAPESAIKFMAYEQIKRLVSGDETLRIHERLVAGSLAG 291
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 300 ATAQFTIYPMEVKTRFLAVGKTGOYSIGYDCAKKILKHESGLGAFYKGYVPMNLGITIPYAG 359
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 292 AIAOSSIYPMEEVLKTRMALRKRTGOYSGMLDCARRILAREGVAAFYKGYVPMNLGITIPYAG 351
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QY 360 IDLAAYELLKSYWLDNFAPKDSVNPVNLGCGALSTCGQLASYPLALVTRMQAOAML 419
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 420 EGSPOLNMVGLFRRIISKEGIPGLYRGITPNFMKVLPAVGISIVYVENMKOTLGVTK 477
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 412 EGAPETVMSLFRHLTLRTGAFGLYRGLAPNFMKVIIPAVSISIVYVENLKITLGVQSR 469
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
  
```

Search completed: August 18, 2002, 09:28:54
 Job time: 474 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 18, 2002, 03:02:13 ; Search time 3254.77 Seconds
(without alignments)
17186.048 Million cell updates/sec

Title: US-09-777-921A-1
Perfect score: 2673
Sequence: 1 ccgcacccgcagcgccgccc.....ataccatgcatgtctctg 2673

Scoring table:
IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: GenEmbl:*
2: gb_ba:*
3: gb_bt:*
4: gb_in:*
5: gb_ov:*
6: gb_ov:*
7: gb_ov:*
8: gb_ov:*
9: gb_ov:*
10: gb_ov:*
11: gb_ov:*
12: gb_ov:*
13: gb_ov:*
14: gb_ov:*
15: gb_ov:*
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18: gb_ov:*
19: gb_ov:*
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21: gb_ov:*
22: gb_ov:*
23: gb_ov:*
24: gb_ov:*
25: gb_ov:*
26: gb_ov:*
27: gb_ov:*
28: gb_ov:*
29: gb_ov:*
30: gb_ov:*
31: gb_ov:*
32: gb_ov:*
33: gb_ov:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	DB ID	Description
------------	-------	-------	--------------	-------	-------------

1	2261	84.6	3259	9	AF123303	AF123303 Homo sapi
2	1389	52.0	3298	4	AF004161	AF004161 Oryzola
3	1138.2	42.6	170026	2	AC013627	AC013627 Homo sapi
4	1136.6	42.5	183037	9	AL390036	AL390036 Homo sapi
5	1126	42.1	159384	2	AL356110	AL356110 Homo sapi
6	657.2	24.6	1089	10	BC022637	BC022637 Mus muscu
7	545.4	20.4	2555	10	BC019978	BC019978 Mus muscu
8	545.4	20.4	2576	10	BC022114	BC022114 Mus muscu
9	543.8	20.3	3334	6	AX092326	AX092326 Sequence
10	498	18.6	3712	9	AB067483	AB067483 Homo sapi
11	495.8	18.5	2857	9	AK054901	AK054901 Homo sapi
12	436	16.3	1929	6	AX338084	AX338084 Sequence
13	403.2	15.1	1294	9	HSMB00506	AL050209 Homo sapi
14	385.4	14.4	2757	9	BC005163	BC005163 Homo sapi
15	332.2	12.4	578	6	AX340224	AX340224 Sequence
16	318.4	11.9	159384	2	AL356110	AL356110 Homo sapi
17	318.4	11.9	188622	9	AL359258	AL359258 Homo sapi
18	306.6	11.5	2089	9	BC001656	BC001656 Homo sapi
19	215.6	8.1	175811	2	AC095336	AC095336 Rattus no
20	187.4	7.0	1843	8	AY056219	AY056219 Arabidops
21	179.6	6.7	27598	3	CEP55A11	272511 Caenorhabdl
22	171.6	6.4	336	6	AX247315	AX247315 Sequence
23	168.8	6.3	400	6	AX247311	AX247311 Sequence
24	165.4	6.2	1473	10	BC004720	BC004720 Mus muscu
25	160	6.0	175811	2	AC095336	AC095336 Rattus no
26	150	5.6	122100	2	AC007328	AC007328 Drosophil
27	150	5.6	136451	2	AC020327	AC020327 Drosophil
28	150	5.6	167342	3	AC093438	AC093438 Drosophil
29	150	5.6	265536	3	AE003541	AE003541 Drosophil
30	128	4.8	57246	8	AB010069	AB010069 Arabidops
31	125.8	4.7	178480	2	AL671921	AL671921 Mus muscu
32	124.2	4.6	116763	8	AT7211	AL163912 Arabidops
33	116.8	4.4	148906	2	AP003629	AP003629 Oryza sat
34	113.4	4.2	188622	9	AL359258	AL359258 Homo sapi
35	98.6	3.7	53002	9	AL390038	AL390038 Homo sapi
36	98.4	3.7	1397	8	AY062478	AY062478 Arabidops
37	97	3.6	1030	8	AF370255	AF370255 Arabidops
38	97	3.6	1414	4	AF370255	AF370255 Arabidops
39	95	3.6	1233	4	BTGDCP	X66035 B. taurus mr
40	89.2	3.3	1719	9	HOMMSCA	M31659 Human GT ml
41	88.6	3.3	194056	9	AL590708	AL590708 Human DNA
42	87	3.3	42143	2	AC011539	AC011539 Homo sapi
43	87	3.3	141291	9	AC010503	AC010503 Homo sapi
44	87	3.3	152195	2	AC016331	AC016331 Homo sapi
45	86.6	3.2	68726	8	AB017063	AB017063 Arabidops

ALIGNMENTS

RESULT 1	AF123303	3259 bp	mrna	linear	PRI 01-FEB-2000
LOCUS	AF123303				
DEFINITION	Homo sapiens calcium-binding transporter mRNA, partial cds.				
ACCESSION	AF123303				
VERSION	AF123303.1	GI:6841065			
KEYWORDS					
SOURCE					
ORGANISM	human.				
REFERENCE					
AUTHORS	Biery, B. and Valle, D.				
TITLE	Cloning and subcellular localization of a human calcium-binding transporter				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 3259)				
AUTHORS	Biery, B. and Valle, D.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-JAN-1999) Pediatrics/Genetics, Johns Hopkins University, 725 N. Wolfe Street PCTB 803, Baltimore, MD 21205, USA				
FEATURES					
source	1. 3259				

D	718	CTTTGGACAGATGATGATAAAGGAAGGAGGTGTCCTCCCTGCTGGAGAGAAATGGGACAA	777
Q	908	cgcatcaaatctgctctctgagacagctglttaattctgggcatalgaacagltacaaga	967
D	778	TGTCATTAAGATGGTCTCTGGAGACGGCGGAAGTCTCGGCTTATGACCACTACAGAA	837
Q	968	gttacttacttgaaagagacaaaatcaggaaactttgagagattatcttcgyltccat	1027
D	838	GTTCGCTACTAGGAGAGACAAAAATATGAGACCTTTGAGAGATTTATTTCCGGTTCCAT	897
Q	1028	ggcttgagcaacttgagcagctctcttgaaatattgattgagcaagaagatttgaaca	1147
D	898	GGCCGAGACACCCGACAGAGCTTATTTCCATGAGAGCTTATGAAAACCAAGCTGGC	957
Q	1088	ttagagcaacttgagcagctctcttgaaatattgattgagcaagaagatttgaaca	1147
D	958	TGTATGACAAATGGACATATCTCTGGAAATATATGACTGTGGCCAAAGATTTGAAATA	1017
Q	1148	tgaaggtcttgagagcttttcaaaaggctatgtcccaatttctttagatcataccta	1207
D	1018	TGAGAGTTTGGAGCTTTTACAAAGGTATATGTTCCAAATTTATGTAGCATATCTTA	1077
Q	1208	tgcaggtcatagatctctgctgtgtatgagctcttgaagtcctatctgctgataattgc	1267
D	1078	TGCAAGCATATAGCCCTTGCTGTATGTAGCTCTTGAAATCCACTGTGGATTAATTTGC	1137
Q	1268	aaaagatctgtaaacccttgagtcacagtgctgtgcgtgagtcggtgcttaccagac	1327
D	1138	AAAAGACTCTGTCAACCTCGAGTTCTGATTTGCTGGGTGTGGTCTTATCCAGAC	1197
Q	1328	ctgtgtcagctgtgcagctacccattgtgcttggtagaactgcgatgcagctcaagc	1387
D	1198	CTGTGGCCAGTTGGGCACACTTCCCTTGCGTTGTGTAGAACACGCAATCAGCTCAAGC	1257
Q	1388	catgttgaaggttcccaagcagctgaattggttggcctcttgcagagatatttccaa	1447
D	1258	CATGCTGGAAGAGAGCCCAACGCTGAACATGTGGGCTCTTTAGAGAAATTAATTTCCA	1317
Q	1448	agaagaataccaggaacttacaagagcatcaccccaacttcatgaagtggtccctgc	1507
D	1318	AGAAAGACTCCAGAGCTTTTACAAAGGACATACCCCAACTTATGAAAGTCTCCGTC	1377
Q	1508	ttagagctcagttatggtgtttcttgaaatatgaagcaaaactttagaggttaaccaga	1567
D	1378	TGTATGACATACGCTACGCTGTATGAAATATGAAGCAAACTTATGAGATACCCAGA	1437
Q	1568	atgaatc -gttcattttcttcttagcctgatatgaattgaacttcaacaactctcgagt	1625
D	1438	GTGATATAGGTTGAGCGGTGTGATCCAGCATTAATTATGAAATCTTCAACATCTGTGAGA	1497
Q	1626	gactcttctcctcgtgaattgaacaagctcatagycaaaagaa-----	1667
D	1498	GAAATGTTCTCTTAATAATTTGCAACATCTGTGGCAAAAAATCCAAACCAAAACAAA	1557
Q	1668	-----gcgtcatttttccacaagaagggaagacgltacaatgltcaactcaaa	1718
D	1558	AAGTGTACTTTTTTTTTTTTTTCCACCAAGAGGAGAACATATCAACATCACTTCAA	1617
Q	1717	cttctgggtcaatataatgacagaaatgltcaaatcatagltttaaagltgtt	1776
D	1618	CATTTGAGTTGAGTTTCCATACACAGAAA -TTCAAGGTCAATAGTTTAAATAACTTTTG	1675
Q	1777	aaaaggtcaacaatctacttacttcttctctaataaact---tgcgaatctgcct	1833
D	1676	GAAA -GCCACAAATTTGACGTATATCTTGTATTAATCTTTTGGCAATCTTAACCTT	1734
Q	1834	gaatccgaatctgaaatgctactgcgtgtgaacaaattglttltgttgaagttat	1893
D	1735	TAGTCTCAATCTCAAAATGATTTTGGTGAACATAATTGTTTGTGTGTGATGAATAT	1794
Q	1894	aaatcaatcaattctattctgggtgtgttaagttatgccagltccttataatt	1953

RESULT	ACOL13627/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	
Db	1795	A-----	AACTTATATTTGATTTAGATATATATCCAGTCTTTTATATTTGATG	1847										
Qy	1954	tctgtt-----	ttatatatttgaagtcttata	1984										
Db	1848	TCCTTTTAAAGCAAAATGATCAGAAACCTCGATATATATTTTAAATATATCTATA	1907											
Qy	1985	gattcttctaattcccttatagaaccaataagaataatcattcattataaatalacc	2044											
Db	1908	GACATCTTCGCACTTCATTTAAATCATATAAGCAAAATCAGCTCAGCTTAAATATGTT	1967											
Qy	2045	ttacagcaaaagcatccaaataagatagatgggtttagtcccttatttcttcagctgaa	2104											
Db	1968	TT-----AAATATGATCCAAATAGATATGAGATTTATATCTTCACCTTTCTTAAAGTGAA	2021											
Qy	2105	tacgaataacacagcttggttggaatttcggaaggaagcgatgaataatattatttcag	2164											
Db	2022	CAGGAATCACAATAGCTAGTGGATTTTAA--GAGAGAGATATAACTATTATTTCGG	2079											
Qy	2165	tggagcatttccattaccacgttaccattatttggttcctggaattacacaaat	2224											
Db	2080	TAGGACACTTTCATTTGCG--TTGCACTGTTAATTTGATTTCTATATATTAATCTGAT	2137											
Qy	2225	ttcag	2229											
Db	2138	GTCAG	2142											
RESULT	3	ACOL13627/c	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE <td>JOURNAL</td> <td>COMMENT</td>	JOURNAL	COMMENT
Db	179026	bp	DNA	Linear	HTG	12-MAR-2000								
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Qy	179026	bp	DNA	Linear	HTG	12-MAR-2000								
Db	179026	bp	DNA	Linear	HTG	12-MAR-2000								
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Qy	179026	bp	DNA	Linear	HTG	12-MAR-2000								
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Db	179026	bp	DNA	Linear	HTG	12-MAR-2000								
Qy	179026	bp	DNA	Linear	HTG	12-MAR-2000								
Db	179026	bp	DNA	Linear	HTG	12-MAR-2000								
Qy	179026	bp	DNA	Linear	HTG	12-MAR-2000								
Db	179026	bp	DNA	Linear	HTG	12-MAR-2000								
Qy	179026	bp	DNA	Linear	HTG	12-MAR-2000								
Db	179026	bp	DNA	Linear	HTG	12-MAR-2000								
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Qy	179026	bp	DNA	Linear	HTG	12-MAR-2000								
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Qy	179026	bp	DNA</											

Oy 1625 tgacatttttcctcgcgaatgaaacaagtcataggcaaaaagaagctgca ttttttcaca 1684
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Db 127832 TGACTTTTCTCCGCAATGGAACAAGTCATGGCAAAGAAGCTGCATTYTTTTTCACA 12773

QY 2525 gaactgtctgttgcataatgagccacaaaggggagaga 2567
 ||||| |
Db 126934 GAACCTGCTGTTCATATGGCAGCACAAAGTGAGAGATA 1268922

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 183037)
AUTHORS Frankland, J.
TITLE Direct Submission
JOURNAL Submitted (06-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquereyes@sanger.ac.uk
requests: clone.requests@sanger.ac.uk

COMMENT

On Sep 7, 2001 this sequence version replaced gi:14456226.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chrl
Rp11-356N1 is from the library RPCR-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.choi.org/bacpac/home.htm
VECTOR: pBACe3.6
This sequence is the entire insert of clone Rp11-356N1 The true
left end of clone Rp11-483113 is at 170175 in this sequence. The
true right end of clone Rp11-320L5 is at 93687 in this sequence.

FEATURES

Source

1. 183037

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="1"

/clone="Rp11-356N1"

/clone_lib="RPCR-11.2"

48723..49036

/note="Sequence from overlapping clone Rp11-320L5
(AL391235). Assembly confirmed by restriction digest."

79012..79019

/note="Sequence from overlapping clone Rp11-320L5
(AL391235). Assembly confirmed by restriction digest."

174215..175019

/note="Cpg island"

/evidence="not_experimental"

BASE COUNT 55819 a 38180 c 35765 g 53273 t

ORIGIN

Query Match 42.5%; Score 1136.6; DB 9; Length 183037;
Best Local Similarity 98.6%; Pred. No. 1.6e-202;
Matches 1167; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

Oy 1385 agccatgttaagaaggtcccaagcgtgaatagtgtgctcttcgaagcaatatttc 1444
|||||
Db 151015 AGCCATGTTAAGAAGGTCCCAAGCAGTGAATAGTGGCCCTTTGACAGCAATATTTC 150956

Oy 1445 caaagaagaatacagacttacagaggtcaccaccaactcatgaagtgctccc 1504
|||||
Db 150955 CAAAGAAGAATACAGACTTTACAGAGGCTACACCCCAAACTTCATGAAGTGCTCCC 150896

Oy 1505 tgcgtgaagcaatcagltatgtgtttatgaataatgaagcaaaccttagagtaacca 1564
|||||
Db 150895 TGCTGTAGCAATCACTATGTGTGTTATGAATAATGAAGCAAACTTTAGAGTAACCA 150836

*Oy 1565 gaatatgtgtgcaatttttgccttaagcctgataatgaaaccttcaacaactctgag 1624

1565 gaatatgtgtgcaatttttgccttaagcctgataatgaaaccttcaacaactctgag 1624

|||||
Db 150835 GAAATGATGTGCATTTTTCCTTAAAGCCTGATTAATGAACCTTCAACATCTCTGAG 150776
Oy 1625 tgactttccctcgaatgaacaagctcagcaagaagctgatttttcaca 1684
|||||
Db 150775 TGACTTTTCCCTCGAATTTGAACAACTATGCAAAAGAGCTGCATTTTTCACA 150716
Oy 1685 aaaggaagacggtatacaatggtcactcaaaccttggcgtaattatctgacacaga 1744
|||||
Db 150715 AAAGGAAGAGGTGTAACTGATGCTCAAACTTTGGCTTAATTTATGTACACAGA 150656
Oy 1745 aatgtcaaatcagtttaagtgttttgaagaagccacaaatatacttattc 1804
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Db 150655 AATGTTCAAAATCATAGTTTAAATGTGTTGAAGAGCCACACATTTATCTTATCTT 150596
Oy 1805 ttcttaataatccctgaatcctcctcgaatccgaatctgaaatctgactgcttga 1864
Db 150595 TTCTTAATAATCCCTGAATCTCTGCTGAATCGGAATCTGAAATGTACTGCTTGA 150536
Oy 1865 acaaaattgttgtgtgtgaagttcaatcaatcaatcttacttccggtgttac 1924
Db 150535 ACAAATTTGTTTGTGTGTGAAGTTTAAATCATTTATCTTTATTTTCGGGTGTTTAC 150476
Oy 1925 gttatgccaattccttataatttgaatttctgttataatttgaatgcttata 1984
|||||
Db 150475 GTTATGCGCAGTCTTATATTTTAAATTTCTGTTTATATTTTGAATGTCTTATA 150416
Oy 1985 gattccttaattcctcctatagaacccaatagaanaatcatcatcattaaatatacc 2044
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Db 150415 GATTCTTTAATTTCCCTATTAGAACCATTTAATGAATCATTTAAATATATAC 150356
Oy 2045 ttacagcaaaagacatccaaataagataggtttatgtcccttatttccctcagctga 2104
Db 150355 TTACAGCAAAAGCATCCAAATAGATATAGGTATATCTTATTTTCTTACCTGAA 150296
Oy 2105 taccgaataaacaagtggtgaatattcgaagggaagatgaatattatattttag 2164
Db 150295 TACGAATGAACACAGTGTGTGAATTTCTGAAGGGAAGATGAATTTATTTATTGAG 150236
Oy 2165 tgggaacttccatatttaccactgttaccattatttgcctgaggtatacctaact 2224
Db 150235 TGGGCACTTTTCCATTTTACACGCTGATCATTTATTTGCTCGAGATATACATAAT 150176
Oy 2225 ttcaatatatactgttataattaccacaacaagaagcaattatttgaagaatccgttat 2284
Db 150175 TTCAATATATATCTGTTTAAATTTCCACACAAAGCAATTTATTTGAAGATTTCCCTTAT 150116
Oy 2285 cctgcattgtccttgaagaagcagcagaagaatatttgaactgtcatcagctctgc 2344
Db 150115 CCTGCCATTTGCTTTGAAAAGCAGCAGGAAAGCAATCTTTGACTTGTATCAGCTTTC 150056
Oy 2345 agaagatcttgttcttcccttgccttgccttgccttgccttgccttgccttgccttgc 2404
Db 150055 AGAGCATCTGTTGTTTCTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTTGTCTT 149996
Oy 2405 gtcaagaagacttcttggagacatctcagtaactgtaaatcttcttcttcttcttct 2464
Db 149995 GTCAAGAAGACTCTTGTGGACCATCTTATGTAACCTGAAATTTCTTTTATATGCAAGA 149936
Oy 2465 agtgaattgatacagaaagatgagtggtgcttatttccctcactggtgtaatactct 2524
Db 149935 AGTGAATTGATCATAGCAAAATGATGTGC -TTATTTCCTCCCTCACTGTTGAATAT -CTTT 149878
Oy 2525 gaactgtctgttgcataatgagcagccacaagaaggagagaga 2567
Db 149877 GAACCTTGCTGTTTCAATATGAGGAGCAACAAGGTGAGAGATA 149835
RESULT 5
AL356110 159384 bp DNA linear HTG 15-MAY-2000
LOCUS AL356110 Homo sapiens chromosome 1 clone RP4-562N20 map p34.1-34.2, ***
DEFINITION SEQUENCING IN PROGRESS ***, 71 unordered pieces.

ACCESSION AL356110
VERSION AL356110.1 GI:9213734
KEYWORDS HTG: HTGS_PHASE1.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159384)
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (14-MAY-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
JOURNAL requests: clonerequests@sanger.ac.uk
On Jul 15, 2000 this sequence version replaced gi:7899229.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: djs62N20
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 112062 bases at least Q40
Consensus quality: 126393 bases at least Q30
Consensus quality: 139133 bases at least Q20
Insert size: 152384; sum-of-contigs
Insert size: 119983; 3.4% error; agarose-fp
Quality coverage: 1.75x in Q20 bases; sum-of-contigs Quality
coverage: 2.22x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 71 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
3401: contig of 3401 bp in length
*
3402 3501: gap of 100 bp
*
3502 5184: contig of 1683 bp in length
*
5185 5284: gap of 100 bp
*
5285 8399: contig of 3115 bp in length
*
8400 8499: gap of 100 bp
*
8500 9995: contig of 1456 bp in length
*
9996 10095: gap of 100 bp
*
10096 12393: contig of 2298 bp in length
*
12394 12493: gap of 100 bp
*
12494 14134: contig of 1641 bp in length
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14135 14234: gap of 100 bp
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14235 15647: contig of 1413 bp in length
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15648 15747: gap of 100 bp
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15748 17013: contig of 1266 bp in length
*
17014 17113: gap of 100 bp
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17114 18234: contig of 1121 bp in length
*
18235 18334: gap of 100 bp
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18335 20824: contig of 2490 bp in length
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20825 20924: gap of 100 bp
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20925 22553: contig of 1629 bp in length
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22554 22653: gap of 100 bp
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22654 28172: contig of 5519 bp in length
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28173 28272: gap of 100 bp
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28273 29368: contig of 1096 bp in length
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29369 29468: gap of 100 bp
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29469 30517: contig of 1049 bp in length
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30518 30617: gap of 100 bp
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30618 31804: contig of 1187 bp in length
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31805 31904: gap of 100 bp
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35405 35504: gap of 100 bp

35505 40678: contig of 5174 bp in length
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51206 52647: contig of 1442 bp in length
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63879 63978: gap of 100 bp
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63979 68912: contig of 4934 bp in length
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68913 69012: gap of 100 bp
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78370 78469: gap of 100 bp
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79869 79968: gap of 100 bp
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81239 81338: gap of 100 bp
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81339 83358: contig of 2020 bp in length
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87480 88655: contig of 1176 bp in length
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88756 89811: contig of 1056 bp in length
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89912 91595: contig of 1684 bp in length
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91596 91695: gap of 100 bp
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91696 93433: contig of 1738 bp in length
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93434 93533: gap of 100 bp
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93534 94622: contig of 1089 bp in length
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94623 94722: gap of 100 bp
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94723 95986: contig of 1264 bp in length
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96087 97205: contig of 1119 bp in length
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97306 102318: contig of 5013 bp in length
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102319 102418: gap of 100 bp
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102419 103670: contig of 1252 bp in length
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103671 103770: gap of 100 bp
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103771 104989: contig of 1219 bp in length
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104990 105089: gap of 100 bp
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105090 106128: contig of 1039 bp in length
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106129 106228: gap of 100 bp
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106229 109170: contig of 2942 bp in length
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109171 109270: gap of 100 bp
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109271 110291: contig of 1021 bp in length
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110292 110391: gap of 100 bp
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110392 113213: contig of 2822 bp in length
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113214 113313: gap of 100 bp
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113314 114986: contig of 1673 bp in length
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114987 115086: gap of 100 bp
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115087 116435: contig of 1349 bp in length
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116436 116535: gap of 100 bp
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116536 117610: contig of 1075 bp in length

[illegible][illegible]

BC022637
LOCUS BC022637 1089 bp mRNA linear ROD 04-FEB-2002
DEFINITION Mus musculus, clone IMAGE:4208509, mRNA, partial cds.
ACCESSION BC022637
VERSION BC022637.1 GI:18490465
KEYWORDS
SOURCE house mouse.
ORGANISM Mus musculus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1089)
Strausberg, R.
Direct Submission
Submitted (01-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Ilife Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mdickpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
Series: IRAX Plate: 43 Row: h Column: 13
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency OK
analysis.
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source Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:4208509"
/tissue_type="Colon, normal, 5 month old male mouse."
/clone_lib="NCI-CGAP_Co24"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
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/codon_start=1
/product="Unknown (protein for IMAGE:4208509)"
/protein_id="AAH22637.1"
/db_xref="GI:18490465"
/translation="GIRSLMRGNGTNVIRKIPETAVKFMAYROYKKLLTEGOKITGE
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LALVTRMQAQATVEGAPQLSWGLVFORIVSKVSGVLRGITPPNFMKVLPAVGISYV
YVENMKOTLGAOK"
CDS
BASE COUNT 293 a 241 c 262 g 293 t
ORIGIN
Query Match 24.6%; Score 657.2; DB 10; Length 1089;
Best Local Similarity 79.1%; Pred. No. 4,6e-113;
Matches 851; Conservative 0; Mismatches 203; Indels 22; Gaps 5;

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Qy 1053 atataccaatggagggttaagaaccagctgctgctgtagcaaaactggcagctctc 1112
Dh 181 ATTACCCCATGGAGGTTTGAAGAACCCGGCTAGCTGTACCCAAACTGGACAATATCC 240
Qy 1113 ggaataatgatctgcgaagaagatttgaacaatgaagctctggagcttttaca 1172
Dh 241 GGATATACGGTGTGTGCAGAGAAAGATTTTGAACACAGAACGCTTTGGGCTTTTACAA 300
Qy 1173 gactatgtcccaattatagblatcaatccttatgacaggaatctctgtgtat 1232
Dh 301 GGCTACATTCCTCAATTTACTAGGACATCTCTTACGACAGCATTTGCTGTGTAC 360
Qy 1233 gactcttgaagccatattgctggtatatttgcagaagatctgtaaaccttgatc 1292
Dh 361 GAGCTTTTGAAGCTTATTTGGCTGGATTAACCTTGGCAAAACATCGGTCAACCTGGCGTG 420
Qy 1293 atgtgtctgctggatgcggtgcttatccagcacctgtgtcagctgacgaacca 1352
Dh 421 ATGGTCTGTGTGAGCTGTGAGCCCTATCCAGACCTGTGTGGCAGCTGGCAGCTACCC 480
Qy 1353 ttgctcttgtagaactgcacatgcagctcaagcattagaaagttcccaagctg 1412
Dh 481 CTGGCTTTGGTGAACTCGCATGCAAGCTCAAGCCAGGATAGAGAGCCCGCAGACTG 540
Qy 1413 aatatgttgctctcttgcagcaatatttccaagaagaataccagcaatttcaga 1472
Dh 541 AGCATGTTGGCTTTTTCAGCAATCTCTCCAAAGAAAGATGTGAGGACTTTTACAGA 600
Qy 1473 ggcatacccacaactcattgaagtgctccctgcctgtagaactcagttgtgtttat 1532
Dh 601 GGCATACCCCAACATTCATGAAAGTGCTCCGGCCGTGGCATACGATATGTGGTGTAT 660
Qy 1533 gaaatatgaagcaaaccttaaggatgaaccagaatga--tgtagcaattttgcttta 1590
Dh 661 GAAATATATGAAAGCAGACCCCTGGGAGTAGCTCAAGATGACCAAGCTTGGCTTTT 720
Qy 1591 gctgttaattgaactttcaacaactctcgagtgagcttttctcctgtaattgaaca 1650
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Qy 1651 agctatgcaaaagaagctgcattttttcacaaaaaggaagcaagylaaatgtgtcac 1710
Dh 773 AGCTATACAAAGGAAGCTG--TTTGCCCTGGCAAAAGGAAGATGTACCGTGATGAC 830
Qy 1711 ttcaaacctttggcctaattatataatgtaacagaatgttcaaatcatagtttaagt 1770
Dh 831 TACAAAGCTTTGGGTTTACGTTTATACCTTCACCGCATGTGTAATGTGTTCAGATA 890
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Dh 891 GTGAAGAAA--CCACAAAATGTACTGTATTTTTCGTGA-----TAGAGATCTCTGC 940
Qy 1831 cctgaatcgaanaactgaaatgtactggtcttgaacaaaattgtttgtgtgtgagt 1890
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Qy 1891 tataatcatlaacttatttcgggtgttaagttatgcacagttccttataat 1946
Dh 1001 TATAAATCACTACCTTTGTTGTGATTTGTTCAAGCTCATGTCAATTTTCTTTT 1056
RESULT 7
BC019978
LOCUS BC019978 2555 bp mRNA linear ROD 22-JAN-2002
DEFINITION Mus musculus, similar to KIAA1896 protein, clone MGC:28954
ACCESSION BC019978
VERSION BC019978.1 GI:18043564
KEYWORDS house mouse.
SOURCE Mus musculus

LOCUS BC022114 2576 bp mRNA linear ROD 28-JAN-2002
DEFINITION Mus musculus, clone MGC:36388 IMAGE:5098924, mRNA, complete cds.
ACCESSION BC022114
VERSION BC022114.1 GI:18380991
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2576)
Strausberg, R.
Direct Submission
Submitted (24-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywicki, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Lisa Prabh, Parvaneh Saedi, Jacqueline Schein, Duane Smalish, Michael Smith, Lorraine Spence, Jeff Stolt, Michael Thorne, Miranada Tsai, Natasia van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRAX Plate: 57 Row: e Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Genomescan gene prediction.
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Location/Qualifiers
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/db_xref="taxon:10090"
/clone="MGC:36388 IMAGE:5098924"
/tissue_type="liver, normal. 5 month old male mouse."
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BASE COUNT 624 a 675 c 710 g 567 t
ORIGIN
Query Match 20.4%; Score 545.4; DB 10; Length 2576;
Best Local Similarity 64.9%; Pred. No. 4.7e-92;
Matches 807; Conservative 0; Mismatches 436; Indels 0; Gaps 0;
QY 316 aggaagaaattttactacggagatgtcaacaagaatggagatcttggaagaat 375
DB 206 AGCAGAAATTTGTCAAGCAGGTGACAGACCTTGATGGGACACTGTTGAAGAGT 265

QY 376 ttatgaagtaacttaaaagacaatgagaagaatgaattgcatcttaagattagaca 435
DB 266 TTGTACATTTACCTCCAAAGATCATGAGAAAAAAGTGAAGCTGGTTCAGAGCTGGACA 325
QY 436 aaaaatagtatgaaaaaatgtagcttcagaattgtccagctctccagaactgtgc 495
DB 326 AAAAGATGATGGTTCGAAATGATGATGATGATGATGATGATGATGATGATGATG 385
QY 496 tgaactttctgaacaaacagagatgtgattctgaacaaatgattgattgagaca 555
DB 386 TCAAGATCTCGAAGACGACGAGGAGAGATTTTAAAGACATGAGATTAAGATGGACGA 445
QY 556 tgaacgtgagactgtaatagtgagagactactcttatttaaccgttcaagacatg 615
DB 446 TGAACATCGACATGGAAGAGATGAGAGATGAGAGATGAGAGATGAGAGATGAGAG 505
QY 616 aggaataatccgtttctggaacaatctcaggaattgacataaggagataagctaa 675
DB 506 CGGAGATCATCTGTTACTGGAGACGACTCGAGATCTTCGATGTCGGTGAAGATCTGAC 565
QY 676 ttccagatgaattcacggaagaaagaaaaaatcccgacaatgtaggacagcttg 735
DB 566 TCCCATGATGATTCACAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 625
QY 736 caggagagcatgtgctgtgctgtctctcgaacaagcactgccccttggacgctgtg 795
DB 626 CAGAGAGTGGGCGACGGGCGAGTTTCCAGAACCTGCACTGCCCTCCGACAGACTGA 685
QY 796 tcatgatgcaggttcacggttcacaaatcagaacaataatgacataattgtgtgttc 855
DB 686 TGTCTCAATGCAAGTCCCAAGCTCCCGCAGCAACAATGTCATGTTGGTGGATTCCAC 745
QY 856 agatgtaaaaagagaggtatccgcgtcgttgaaggaagaaatgtaacaagcttca 915
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QY 916 aaattgctcttgagacagcgtttaattctggtgcatatgacaagataagaagtact 975
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DB 926 CCAATTGCGCAGAGTAGCATTTACCAATGAGAGGTTCTGAAGACCCGATGGCCGCGA 985
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QY 1156 tggagagcttttcaaaagcctatgttcccaattattatagatcatccttatgagca 1215
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QY 1276 ctgtaaacccctgagatcatgtgttgcgtgagatgcgtgtccttaccagaacacctgt 1335
DB 1166 GTGCAAGACCCCGGT 1225
QY 1336 agctgacagctacccaatgtgtgttgtagaactctgcatgcaggtcacaagcattgag 1395
DB 1226 AGCTGGCACCTACCCACTAGCCCTGTGTGAGGAGCCCGAGGACGAAGCCCTCCATT 1285
QY 1396 aaggttcccaacagcgtgaataatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1455
DB 1286 AGGCGCAGCTTGAGGTTAACATGAGACGCTTTCAAAACAGATTCTCGGACTAGGG 1345
QY 1456 taccagagacttcaagagcatcaccccaactcatgaaggtgtcctctgtgttagca 1515

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RESULT	9		
AX092326			
LOCUS	AX092326	3334 bp	DNA linear PAT 23-MAR-2001
DEFINITION	Sequence 57 from Patent WO0116318.		
ACCESSION	AX092326		
VERSION	AX092326.1	GI:13444477	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Eumalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 3334)		
AUTHORS	Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,		
	Goodwini,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and		
	Wood,W.I.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding		
	the same		
JOURNAL	Patent: WO 0116318-A 57 08-MAR-2001;		
FEATURES	Genentech, Inc. (US)		
source	location/Qualifiers		
	1..3334		
BASE COUNT	788 a 848 c 983 g 715 t		
ORIGIN			
Query Match	20.3%; Score 543.8; DB 6; Length 3334;		
Best Local Similarity	64.8%; Pred. No. 9,9e-92;		
Matches 806; Conservative	0; Mismatches 437; Indels	0; Gaps	0;
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Qy	376	ttagtaagtaacctaaagccatgagaagaatgaatgtgcatltaagaattagaca	435
Db	275	TTGTCTATTATCTCCAAAGATCATGAAAMAACTGAGCTGGTGTTAAGATTGTGACA	334
Qy	436	aaaataatgatgaaataattgaggtctcagaattgtcgaagctctccagacacttggtc	495
Db	335	AAAAGATATGTGACCACTTGTGACGCCAGAGATCATGCAAGTCCCTGCGGGACTTGGGAG	394
Qy	496	tgactatcttcgacaaacaagcagagtgtatcttcaagaatltgattgttgaatggacaa	555
Db	395	TCMAAGTATCTGCAAGCGACGAGAAAATTTCTCAAGACATMGATTAAMAAAGGACGA	454
Qy	556	tgaagtgagacttggaatgtgagagactactcttattatcctgttgaagaatcag	615
Db	455	TGACCATGCACTGGAACGAGTGGAGGACTACCTCCTCCACCCCGTGAAMAACTATC	514
Qy	616	aggaataatccglttccttgaaacattccacaggaattacatagaggatgacttaacta	675
Db	515	CGAGATCATCTCTACTGTGGAAGCATTCACAGATCTTTATGTGGGTGAGATTAACGG	574
Qy	676	ttccagaatgaattcacgagaagcagaaaaaattccggaacatggtgaggaagcctttg	735
Db	575	TTCCCGATATGTTCCACAGTGGAAGCAACAGCGGGATGTGTGGTGAACACCTGTGTC	634
Qy	736	caggaagcaatgctgtgtgtctctcagaaacagcaactcccttggacgcttgaanaa	795
Db	635	CAGGAGTGGGGCAGGGGCCGTAATCCAGAACTGCAAGGCCCCCTGGACAGGCTCAAGG	694
Qy	796	tatgatgaaggttccacggttccaaatcagacaaatagacatattgtgtgcttccag	855

[illegible]

sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp586G0123) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY. Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <http://www.mips.biochem.mpg.de/proj/cDNA/>.

FEATURES

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/db_xref="taxon:9606"
/clone="DKFZp586G0123"
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25..315
/gene="DKFZp586G0123"
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POLYA_site 1278
BASE COUNT 408 a 174 c 196 g 516 t
ORIGIN

Query Match 15.1%; Score 403.2; DB 9; Length 1294;
Best Local Similarity 96.7%; Pred. No. 1.9e-65;
Matches 433; Conservative 0; Mismatches 13; Indels 2; Gaps 2;

OY 2120 tgggtgaatttcgaaggaagtgatgaataatataatttcgaatggaactttccat 2179
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DB 1 TCGTGGAAATTTGGAAGGAGATGATGAATATATTATTTCAGTGGCATTTCAT 60
OY 2180 ttaccacgtaccattatttggtccctggaattatacaactaatttcagtatattacg 2239
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DB 61 TTTACCACTGTACCAATATTGTTGCTCTGAGTTTATACACTAATTTTCAGTATATTAC 120
OY 2240 ttaaataccacaacaagaacattatattgaagaattccgttatccatcgcttg 2299
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DB 121 TTAATATACCAACACAGCAATTTATTGAAAGATTCGTTATCCCTGATTCGCTTTC 180
OY 2300 aaaagcagcaggaacgaataattttgactgtaacagctctgcagaagcatttggtt 2359
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DB 181 AAAACGACGAGGAAAGAAATCCCTTGAAGTGTATCAGCTCTGCAGACATCTTGT 240
OY 2360 tcccttgctctgtttcctacatttgaatcagaattccgttttgctggaagacttt 2419
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DB 241 TCCCTTGTCTTGTCTTCTACCTTTGATACAGATCCGTTTATGTCAGAAAGACTTCT 300
OY 2420 tgggaacattcttaagtaactgaatttccttttaattgcaatgaatggaatgacatg 2479
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DB 301 TCGGAACATTTCTTAACTGAATTTCTTTTAAATTCGATGAAGTGGATGATCATG 360
OY 2480 agcaagtgatgggttatttctccctcactggtggaataatccttgaactgctgttgc 2539
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DB 361 ACCAATGATGATGTC- TTATTTCCTCCCTCAGCTGTGAATAT-CTTTGAACCTGCTGTTTC 418
OY 2540 aatatggcagccacaagaaggagaga 2567
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DB 419 AATATGGCAGCAACAAGGTGAGAGATA 446

RESULT 14
BC005163

LOCUS BC005163 2757 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, clone IMAGE:3530123, mRNA, partial cds.
ACCESSION BC005163
VERSION BC005163.1 GI:13477372
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2757)
AUTHORS Strausberg, R.
JOURNAL Direct Submission
Submitted (26-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadane@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Kettelman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRL Plate: 11 Row: e Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

FEATURES

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VFLLACSTMSSTGQSLASYPDLAVRTMQOASIEGAPEVTMSLSLFKHILRTGAFG
LYRGLAPFMKRVIPAVSISVYVEELKTLTAVQSR"
BASE COUNT 599 a 710 c 843 g 605 t
ORIGIN

Query Match 14.4%; Score 385.4; DB 9; Length 2757;
Best Local Similarity 64.1%; Pred. No. 4.6e-62;
Matches 581; Conservative 0; Mismatches 326; Indels 0; Gaps 0;

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DB 19 TTGATGTGGTGAGATCTTAACGGTCCCGATGAGTTCACAGTGGAGAGGACGAG 78
OY 712 gacaatggtggaggaagcatttggcagaaggatgctggtgctgcttcgaacaagga 771
|||||
DB 79 GGATGTGTGGAGACACCTGCTGGCAGAGGCGGCGGATTCACAGAACCTGCA 138
OY 772 ctgccccttgacgcgtcgaataatcatgatcatgacaggttcaaatcagaanaa 831
|||||
DB 139 CGGCCCCCTGGACAGCGCTCAAGGTGCTCATGAGTCCATGCTCCCGACACACACA 198

Oy	832	tgaacatacttttgggtggttcctgacagatggytaaaagagagytatccgcctgctttga	891
Db	139	tgggcattgttgggtggcttctacctaagatgatctcgaaagagagggcccgaggtactcttggc	258
Oy	892	ggggaaatcgtacaaactcatalcaaatctgtccctgagacagctgtttaatcttggcat	951
Db	259	ggggcaaatggcatcagctcctctcaaaattggccccggaatcagccattcaattcaggcct	318
Oy	952	atgaacagtcacaagaagtlactacttactgaagaagacaataatagaacatlttgagat	1011
Db	319	atgagcacaatcagaagcgcttgttggtactgacacagaaactcttgagatcattcacagagac	378
Oy	1012	ttattctcgttccatctgctgtgagaaactgcagactttatatatccaatgtagtla	1071
Db	379	tttggcagaggtctcttggcagagggccatccgccaagacagatcttaaccatgtgaggtcc	438
Oy	1072	tgaaacaccagctgtgctgttagcacaactctggcagctactctcgtgaatatatgttgc	1131
Db	439	tgaaacaccggatgagcgttcgggaagaaagccagctactcagaaatgcttgacactgcgca	498
Oy	1132	agaagatlttgaanaacatgaagcttggagacttlttacaaggtcgtatgttcccaattat	1191
Db	499	ggagagatccttgagccagagagaggggctgcccgccttctacaaagagctatgcccacatgc	558
Oy	1192	tagtatcatcatccttatgcatgagctagaatctgtcctgtgtatgagctccttgaagtcatt	1251
Db	559	tgggcattatccctcttatgtccgcatccgcatcttgacatgtatagacagcctcaagaatgctt	618
Oy	1252	ggtcgtgataatlttgcacaagaatctctgaaacccctgtagtcatagttctgtcgtgatgcg	1311
Db	619	ggctgcacacactgtatgcagatgaacagccgggagacccggcggtgtttgtgctcgtggctgtg	678
Oy	1312	gtgccttatccagcaacctgtgtgaactgtgcccagctaccatctggttltgtlgaactc	1371
Db	679	gcacctatctccagtaacactgtgtggccagctgagccagcttacccttgccctagtcagagacc	738
Oy	1372	gcattcagagtcacagccactgtttagaaggttltcccaacagctgaatctgttggcccttcc	1431
Db	739	ggatccagagccgacacacctcttatgagggcgctccggaagtgacatgagacacactctttca	798
Oy	1432	gacgaattatltccaagaagaatataccaggaacttatacagaagcatcaccccaacttca	1491
Db	799	aacatattccttgaggagccagagggcgcttcgggctgttacaagggcgctggcccccaattca	858
Oy	1492	tgaagtgctccctcgtcgtttaggcacatcagttatgtgtttatgtaaaatatgaagcaactt	1551
Db	859	tgaaggtcatctccagctgtgagacatcagctgagtgcttacgagaaactgaaagatcaccc	918
Oy	1552	tagagat 1558	
Db	919	tggcgct 925	
RESULT 15			
AX340224			
LOCUS	AX340224	578 bp	DNA linear PAT 10-JAN-2002
DEFINITION	Sequence 471 from Patent WO0196388.		
ACCESSION	AX340224		
VERSION	AX340224.1	GI:18136206	
KEYWORDS	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1 (sites)		
AUTHORS	Jiang,Y., Harlocker,S.L. and Secrist,H.		
TITLE	Compositions and methods for the therapy and diagnosis of colon cancer		
JOURNAL	Patent: WO 0196388-A 471 20-DEC-2001;		
FEATURES	CORIXA CORPORATION (US)		
source	Location/Qualifiers		
	1..578		

BASE COUNT	167 a	98 c	88 g	222 t	3 others
ORIGIN	/organism="Homo sapiens" /db_xref="taxon:9606"				

Query Match	12.4%;	Score 332.2;	DB 6;	Length 578;
Best Local Similarity	96.0%;	Pred. NO. 3.2e-52;		
Matches 362;	Conservative 0;	Mismatches 13;	Indels 2;	Gaps 2;

Oy	2191	acatttatcttgatctcccgagagattacacactaaattttcaglatatattacgcttgaattacca	2250
Db	1	ACCAATTATTTGGTCTCGAGATTATACCTAAATTTTTCATATATTACTGTTAAATTACCA	60
Oy	2251	acacaaggaacatttatcttgaagaattccglttaaccctgcatttgctttgaaagaacagag	2310
Db	61	ACACAAAGCAATTATTTTGAAGAATTCCTGTTATCTCTGCATTTGCTTTGAAGAAGCAGAG	120
Oy	2311	gaagaagaatttttgacttgatlcagcgtctctgcagaagacacttgattcccttgctcct	2370
Db	121	GAACAGAAATCCCTTGACTGTATCAGCTTCTGCAAGACATCTTGTTGCTTTGCTTGTCT	180
Oy	2371	tgtgttcctacatttgaatcaaacattccgltttagtcagaagaagactcttgaggaccact	2430
Db	181	TTGTTTCCCTACCTTTTGAATTCAGATTCGGTTTAGTCAGGAAGACCTCTGGGACCAATTC	240
Oy	2431	ttagtaaacctgaaattctcttctttaaattgcatgaatggatgatgcataagaaagtga	2490
Db	241	TTAGTAACCTGAATTTCTTTTAAATTGCAATGAATGATGATTCATCATGACGAATATGATG	300
Oy	2491	ggcttatcttctccctcaactcgtgtaatatcccttgaactctgctgttgtaatatggcgag	2550
Db	301	TGC-TTATTTCTCCCTCACAGTTGAATAT-CTTGAACATTCGCTGTTTCAATATATGGCAG	358
Oy	2551	ccacaaaggggagagaga	2567
Db	359	CACAAAGGTAGAGATA	375

Search completed: August 18, 2002, 08:23:49
Job time: 19296 sec

Db 1663 gggagaagtgtaacaatggtccattccaaactttgggtcaaatatataatgtaacagaat 1722
QY 1748 gtccaataacatagtttaattggtttgaaagggcacacaattacttaacttttc 1807
Db 1723 gtccaataacatagtttaattggtttgaaagggcacacaattacttaacttttc 1782
QY 1808 ttaataatccgtgaatctctgcccgaatccgaatctggaatctgaaatgtaactgttgaac 1867
Db 1783 ttaataatccgtgaatctctgcccgaatccgaatctggaatctgaaatgtaactgttgaac 1842
QY 1868 aaattgtttgtgtgtgtagtaataatcaatcaattcttaattcgggtgttccgct 1927
Db 1843 aaattgtttgtgtgtgtagtaataatcaatcaattcttaattcgggtgttccgct 1902
QY 1928 tatggcaagttcccttaatttaattctctgtttatattatattggaatgtccttaagat 1987
Db 1903 tatggcaagttcccttaatttaattctctgtttatattatattggaatgtccttaagat 1962
QY 1988 ttcttaaatcttccatagaaccatlaataagaanaatcatattacattlaaataataccta 2047
Db 1963 ttcttaaatcttccatagaaccatlaataagaanaatcatattacattlaaataataccta 2022
QY 2048 cagcaaaagcatcccaataaataagtaggtttatgtccctaatttcccttcagctgaatc 2107
Db 2023 cagcaaaagcatcccaataaataagtaggtttatgtccctaatttcccttcagctgaatc 2082
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QY 2468 ggaatgataatagaagaatgagtggtttattcttccctcaactggtgaatctcttga 2527
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RESULT 2

AAC77660
ID AAC77660 standard; cDNA; 1090 BP.XX
AC AAC77660;XX
DT 08-FEB-2001 (first entry)XX
DE Human cancer associated gene sequence SEQ ID NO:54.XX
KW Human: cancer associated gene; cancer antigen; detection; cancer;KW
diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;KW
antidiabetic; antidiabetic; antineumatic; antidiabetic; antiviral;KW
antiinflammatory; antithyroid; antiallergic; antibacterial; cardiac;

KW dermatological; neuroprotective; thrombolytic; coagulant; nootropic;
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening; ss.
OS Homo sapiens.
PN MO200055350-A1.
PD 21-SEP-2000.
PF 08-MAR-2000; 2000MO-US05882.
PR 12-MAR-1999; 99US-0124270.
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Ruben SM;
DR WPI, 2000-587533/55.
DR P-PSDB; AAB43451.
PT Novel isolated nucleic acids comprising sequences encoding peptides
PS useful for treating or diagnosing e.g. cancer -
XX
XX Claim 1; Page 651; 2352pp; English.

CC AAC77607 to AAC78448 encode the human cancer associated proteins given
CC in AAB4398 to AAB44239. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vulnerary; immunomodulator;
CC antidiabetic; antidiabetic; antidiabetic; antidiabetic;
CC antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiac; thrombolytic; coagulant;
CC nootropic; vasotropic; antipsoriatic and antiangiogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating
CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB44240 represent sequences used in the exemplification of
CC the present invention.

SO Sequence 1090 BP; 328 A; 175 C; 174 G; 411 T; 2 other;

Query Match 35.3%; Score 943.6; DB 21; Length 1090;
Best local Similarity 98.2%; Pred. No. 3.9e-202;
Matches 996; Conservative 0; Mismatches 14; Indels 4; Gaps 4;

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Db 1 gagtaaccagaatgatgttgcatttttgccttagctgcgtgaataatgaaacttcaaca 59
QY 1615 atctctgagtgacttttctcctcgatggaacaagctatagggcaagaagctcat 1674
Db 60 atctctgagtgacttttctcctcgatggaacaagctatagggcaagaagctcat 119
QY 1675 ttttttcaaaaagggaagacggtlaaacaatgctacttcaaaacttttgggttaattata 1734
Db 120 ttttttcaaaaagggaagacggtlaaacaatgctacttcaaaacttttgggttaattata 179
QY 1735 tgtacacagaatgctcaaaatacatagtttaattgtttttgaaaggccacacattat 1794
Db 180 tgtacacagaatgctcaaaatacatagtttaattgtttttgaaaggccacacattat 239

QY 1795 acttatactttcttaataatccctcgaactcctgcctt-gaatccgaatctgaaatg 1853
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Db 240 acttatactttcttaataatccctcgaactcctgccttgcctgaaatctgaaatg 299
QY 1854 tactgcttgaaacaaattgttctgtgtgtagagttataatcattcattc 1913
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Db 300 tactgcttgaaacaaattgttctgtgtgtagagttataatcattcattc 359
QY 1914 ggggtgttaagttatgacaggttcccttataattcattcattcattcattc 1973
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Db 360 ggggtgttaagttatgacaggttcccttataattcattcattcattcattc 419
QY 1974 atgcttatagattcttcttaattccttcttataagaccattataatcattcattc 2033
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Db 420 atgcttatagattcttcttataattccttataagaccattataatcattcattc 479
QY 2034 taaatacttaccagcaaaagcatccaataagtagagttatgcttatttctc 2093
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Db 480 taaatacttaccagcaaaagcatccaataagtagagttatgcttatttctc 539
QY 2094 ttccagctgatacgaatgacacagtggtggaattctgaaggagtagataat 2153
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Db 540 ttccagctgatacgaatgacacagtggtggaattctgaaggagtagataat 599
QY 2154 attactcagtgagcactttccatttaccacgttacattatttggctcctgagtt 2213
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QY 2214 ataacactatttcagatatactgtttaattaccacacaggaatttattgaaag 2273
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Db 660 ataacactatttcagatatactgtttaattaccacacaggaatttattgaaag 719
QY 2274 attcggttatctcgcctcattgcttctgaaagacaggaagaatttttgaattgta 2333
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Db 720 attcggttatctcgcctcattgcttctgaaagacaggaagaatttttgaattgta 779
QY 2334 tcagctctcagagacacattgttcttcttcttcttcttcttcttcttcttcttct 2393
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Db 780 tcagctctcagagacacattgttcttcttcttcttcttcttcttcttcttcttct 839
QY 2394 attcggttatctcgcctcattgcttctgaaagacaggaagaatttttgaattgta 2453
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Db 840 attcggttatctcgcctcattgcttctgaaagacaggaagaatttttgaattgta 899
QY 2454 taattgcatgaagtgattgatactgagcaagtgatggcttatttctcctcactggt 2513
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Db 900 taattgcatgaagtgattgatactgagcaagtgatggcttatttctcctcactggt 958
QY 2514 gaatactcttgaactgctgttggcaatgagcagcccaaaaggaggagata 2567
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Db 959 gaatactcttgaactgctgttggcaatgagcagcccaaaaggaggagata 1011

RESULT 3
AA163830
ID AA163830 standard; cDNA; 757 BP.
XX
AC AA163830;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 38.
XX
KW Human; antiarthritic; antirheumatic; antiproliferative; vasotropic;
cerebroprotective; nootropic; neuroprotective; immunosuppressive; antiviral;
fungicide; ophthalmological; cytostatic; immunosuppressive; nootropic;
neuroprotective; antiallergic; hepatotropic; antidiabetic;
antiinflammatory; antileuc; vulnery; anticonvulsant; antibacterial;
cardiovascular disorder; gene therapy; cancer; immune disorder;
cardiovascular disorder; neurological disease; infection; human; ss.
OS Homo sapiens.

XX
PN W0200155308-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01309.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209657.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0217496.
PR 26-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 14-AUG-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 18-AUG-2000; 2000US-0225759.
PR 22-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 23-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0227809.
PR 01-SEP-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 06-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.

PR	17-SEP-2000	2000US-0235836
PR	26-SEP-2000	2000US-0236327
PR	29-SEP-2000	2000US-0236367
PR	29-SEP-2000	2000US-0236368
PR	29-SEP-2000	2000US-0236369
PR	29-SEP-2000	2000US-0236370
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PR	02-OCT-2000	2000US-0237039
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PR	13-OCT-2000	2000US-0239937
PR	20-OCT-2000	2000US-0240960
PR	20-OCT-2000	2000US-0241121
PR	20-OCT-2000	2000US-0241175
PR	20-OCT-2000	2000US-0241176
PR	20-OCT-2000	2000US-0241178
PR	20-OCT-2000	2000US-0241808
PR	20-OCT-2000	2000US-0241809
PR	01-NOV-2000	2000US-0244617
PR	08-NOV-2000	2000US-0246474
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PR	08-NOV-2000	2000US-0246476
PR	08-NOV-2000	2000US-0246477
PR	08-NOV-2000	2000US-0246527
PR	08-NOV-2000	2000US-0246528
PR	08-NOV-2000	2000US-0246532
PR	08-NOV-2000	2000US-0246609
PR	08-NOV-2000	2000US-0246610
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PR	17-NOV-2000	2000US-0249210
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PR	17-NOV-2000	2000US-0249214
PR	17-NOV-2000	2000US-0249215
PR	17-NOV-2000	2000US-02493216
PR	17-NOV-2000	2000US-02493217
PR	17-NOV-2000	2000US-02493218
PR	17-NOV-2000	2000US-0249244
PR	17-NOV-2000	2000US-0249245
PR	17-NOV-2000	2000US-0249264
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PR	17-NOV-2000	2000US-0249289
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PR	05-DEC-2000	2000US-0256719
PR	06-DEC-2000	2000US-0251479
PR	06-DEC-2000	2000US-0251856
PR	08-DEC-2000	2000US-0251868
PR	08-DEC-2000	2000US-0251869
PR	08-DEC-2000	2000US-0251989
PR	11-DEC-2000	2000US-0254097
XX	03-JAN-2001	2001US-0239678
XA	(HUMA-) HUMAN GENOME SCI INC	

PI Rosen CA, Barash SC, Ruben SH;
XX WPT; 2001-488781/53.
DR P-PDSB; AAM43524.
XX
PT New isolated nucleic acids and polypeptides, useful for diagnosing,
XX treating and/or preventing human diseases and disorders -
PS
XX Claim 1; SEQ ID NO 38; 664pp + Sequence Listing; English.

CC The invention relates to human polynucleotides (AA153803-AA164012) and
CC the encoded proteins (AAM43497-AAM43660) useful for preventing, treating
CC or ameliorating medical conditions e.g. by protein or gene therapy. The
CC genes were isolated from a range of human tissues disclosed in the
CC specification. The nucleic acids, proteins, antibodies and (ant)agonists
CC are useful in the diagnosis, treatment and prevention of: (a) cancer
CC e.g. breast and ovarian cancer and other cancers of the adrenal gland,
CC bone, bone marrow, breast, gastrointestinal tract, liver, lung, or
CC urogenital; (b) immune disorders e.g. Addison's disease, allergies,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus,
CC Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.

XX
XX Sequence 757 BP; 214 A; 154 C; 209 G; 173 T; 7 other;

Query Match	27.3%	Score 730.8	DB 22	Length 757
Best Local Similarity	96.4%	Prod. No. 2.1e-154		
Matches 743	Conservative 3	Mismatches 8	Indels 1	Gaps 1
QY 100	gtgactcttcctggccagagccgcctctgcctctcgggacattgttcgctgcgtcggagact	159		
Db 2	gtgacttctctcggccagagcgtctctgcctctcgggacattgttcgctgcgtcggagact	61		
QY 160	tccgcctgcgccacgcgcgcctctgcagagacgcggagccgacgcgcctacggagacctct	219		
Db 62	tccgtctgcgccacgcgcgcctctgcagagacgcggagccgacgcgcctacggagacctct	121		
QY 220	tccagcgacttgcacccgcgaatctgggagcagagctgtgtgcacatcgcgcgacttgcagaggggc	279		
Db 122	tccagcgacttgcacccgcgaatctgggagcagagctgtgtgcacatcgcgcgacttgcagaggggc	181		
QY 280	tcaaggaacctgggacatccctctcggccagagacgcgcggagagaaatttctaactcggag	339		
Db 182	tcaaggaacctgggacatccctctcggccagagacgcgcggagagaaatttctaactcggag	241		
QY 340	atgtcaacaagaatctggagagctggaattttgaagaatttatgaagtaaccttaagaacatg	399		
Db 242	atgtcaacaagaatctggagagctggaattttgaagaatttatgaagtaaccttaagaacatg	301		
QY 400	agaagaataatgaatcttgcatttaagaagtttagacaaaaataatgaatggaaaaatttgag	459		
Db 302	agaagaataatgaatcttgcatttaagaagtttagacaaaaataatgaatggaaaaatttgag	361		
QY 460	cttcggaatttgcagcgtctccaggaacatgggtcctactattctgaacaacaagcag	519		
Db 362	cttcggaatttgcagcgtctccaggaacatgggtcctactattctgaacaacaagcag	421		
QY 520	agttgattcttccaaagcatgagttgtagtggacaaatgacagtggacttggaaatgaa	579		
Db 422	agttgattcttccaaagcatgagttgtagtggacaaatgacagtkgacatcgaaatgaa	481		
QY 580	gagactactcttattattatccctgttacaagacatggagaaattatccgttcttggaaac	639		
Db 482	gagactactcttattattatccctgttacaagacatggagaaattatccgttcttggaaac	541		
QY 640	attccacaggaattacataaggaatgaacttaacttcccaatgaatattcaaggaagacg	699		

Db 542 attctacagggaattgaactaagggaatagcttaactatcccgatgaaltccaggaagacg 601
Qy 700 aaaaaaacccgacaatgctggagggcagcctttggcagggagcatctgtctgtct 759
Db 602 aaaaaaacccgacaatgctggagggcagcctttggcagggagcatctgtctgtct 661
Qy 760 ctggaacaagcactgcccctttgacgcgtctgaaatcatgatcaggttcaac 819
Db 662 ctngacaagcactgcccctttgacgcgtctgaaatcatgatcaggttcaac 720
Qy 820 aatcagacaatgaacatattgttgcttca 854
Db 721 aatcagacaatgaacatattgttgcttca 755

RESULT 4
AAS31626
ID AAS31626 standard; cDNA: 757 BP.
AC AAS31626;
XX
DT 04-DEC-2001 (first entry)
XX
DE cDNA encoding novel human calcium-binding protein #50.
XX
KW Human; calcium-binding protein; calcium flux; neurological disease;
KW immune dysfunction; digestive disorder; neoplastic disease;
KW blood disorder; infectious disease; gene therapy; immunosuppressive;
KW antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
KW virucide; ss.
XX
OS Homo sapiens.
XX
PN WO200155304-A2.
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01302.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-019874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
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PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.

PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.

DE	Skin cell cDNA, SEQ ID NO: 454.
XX	
KM	Mouse, skin cell; cytostatic; antiinflammatory; anti-HIV;
KW	neotropic; neuroprotective; vulnery; immunomodulatory; vaccine;
KM	keratinocyte growth stimulation; cancer; angiogenesis inhibition;
KW	inflammation; neurological disease; ss.
XX	
OS	Mus sp.
XX	
PN	WO200069884 -A2.
PD	
XX	23-NOV-2000.
PF	
XX	15-MAY-2000; 2000WO-NZ00075.
PR	
XX	14-MAY-1999; 99US-0312283.
PA	(GENE-) GENESIS RES & DEV CORP LTD.
XX	
PI	Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;
XX	
DR	WPI: 2001-007495/01.
XX	P-PsDB: AAB56023.
XX	
PT	New isolated polynucleotide used in the identification of genetic
PT	disorders and encoding polypeptides used for treating inflammatory
PT	disease, cancer and neurological diseases -
PS	Claim 1; Page 344-345; 352pp; English.
XX	
CC	The present polynucleotide encodes a polypeptide which is expressed in
CC	mammalian skin cells. The polypeptide is useful for stimulating
CC	keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC	modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC	tumours, modulating skin inflammation, stimulating the growth of
CC	epithelial cells, inhibiting the binding of human immunodeficiency virus
CC	(HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
CC	neurological diseases. The polynucleotide can be used as a marker, in
CC	the identification of genetic disorders, and for the design of
CC	oligonucleotides for examining expression patterns.
XX	
SO	Sequence 1808 BP; 419 A; 473 C; 533 G; 383 T; 0 other:
	Query Match 20.4%; Score 545.4; DB 22; Length 1808;
	Best Local Similarity 64.9%; Pred. No. 1.4e-112;
	Matches 807; Conservative 0; Mismatches 436; Indels 0; Gaps 0;
OY	316 agggagaaattttctactctgagatgtccaagaatgaggagtgttgaagaat 375
Dd	208 agcagaataatttggaacaggtgcgaagaccttgatgaggaaacttgaaagagt 267
OY	376 ttatgaagtaacttaaacacatggaagaanaatgaatatgcatctaagattgaaca 435
Dd	268 ttgtcatctactcccaagatcatggaaaaaaatctaggtgtgttc aaagagtcggaca 327
OY	436 aaaataatgatygaaaatltgaggtctcagaatatgtccaggtctctccagacatggttc 495
Dd	328 aaaagaatgatgtcgaaatcgatgtgccagagatcatgaaatgcagtcctcgtcgagccttggtg 387
OY	496 tgacattctggaaaaaagaagcaggttgatcttcaaagcattgatgttgttgagaca 555
Dd	388 tcaagatctcggaaacagaacgagcgagaagaatcttcaagcagatgataagaatgacaca 447
OY	556 tgcagctgagtgatgaatgaatgagaagcactactttaaattcctctgttaagaacatgy 615
Dd	448 tgcaccatgcagtgcgaagcaggtgagggacttacacacctctcgtcacacctgtggagaacatcc 507
OY	616 aggaatatatccgtttctcgaaaccttctacaggaatgacatbaaggtatgcttaacta 675
Dd	508 cggaatcatcctcgtcgtgaaagacctgcagacatcttcgaatgtcgttgagaatctgcagc 567
OY	676 ttccagatbaattcacggaagcagaaaaaaatccggaacatggtggaagcagccttttg 735

Db	568	lcccaagagaa	cttccacag	tgtgagga	gagcagac	gagcgtgga	ctgtcgtg	gagagcc	ccgtgtg	627
Qy	736	caggagagat	tgtcgtgtgt	ctctctcga	caagcac	ctccccct	tgtgac	cgcttgaa	aa	795
Db	628	caggagag	gtgagcgag	gttcacga	acctgcac	ctccccct	gtgacag	cgatgaa	g	687
Qy	736	tcatgagcag	gttccacg	gttcaaat	ctgcagaca	aaatgaac	tattgtgt	cttgcac	855	
Db	668	tgtcctcag	gtcaggtcc	ctcccgac	caacacac	atctgtc	gtatgag	gtgatcaac	747	
Qy	856	agatgtgaa	agaagaggt	gtatccgc	ctgcgtt	gtgaggg	aaatgtg	tccaacgt	catca	915
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Qy	916	aaattgtc	ctcctaga	cagcgtgt	taattct	ctgtgcata	tgaagac	agtaaga	agttaact	975
Db	808	aaattgtc	ccctgag	ctgcgcata	caaatctt	cagcatat	gacagat	gtgaa	acgtcttgc	867
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Db	868	gtatgtac	gacagaa	cgcgtg	agatcc	acgaagag	ctgtgtg	caagc	gtccctgtgc	927
Qy	1036	caactgcac	gaactttat	atatac	atgagat	gtatga	aaacagc	agcgtcgtg	ctgtgaa	1095
Db	928	ccattgtc	ccagagtag	atctacc	aaatgag	gttctgtg	aaagcc	gaatgtgc	gtgcgga	987
Qy	1096	aaactgtg	cagta	ctctgga	atata	gatgtgtg	gcagaaga	attttga	aacatga	agct 1155
Db	988	aaacagac	agaaatc	ccgcgat	ctgtgac	gtgtgc	agagaggt	ctctgtg	ctaaagag	gtg 1047
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Qy	1276	ctgtaaac	ccgtgggtat	gtgtgtgt	ctgtgag	gtgtgtgc	cttatcc	agac	ccgtgtgc 1335	
Db	1168	gtgcagac	cccggtgt	cttccgtgc	ctgtgc	gtgtgtat	ctctcc	agta	cttctgtgc 1227	
Qy	1336	agctgtg	ccagatca	cccatctgt	cttgtg	aaactgc	atgcata	gtgac	gacatgtag 1395	
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Qy	1336	aaggttcc	caagcag	ctgtat	atgtgtgt	gcctcttc	tcgacga	atttcc	aaagaagaa 1455	
Db	1288	agggctgc	acactgt	agatc	atagacat	cttccaa	aaagattct	gtgc	agctgaggg 1347	
Qy	1456	taccagga	cttaca	agagcat	catccca	acattct	gaaggtgt	ctccctgt	gtgaa 1515	
Db	1348	cccttggc	ctctac	cggtggct	gtgccc	caactct	atgaaggt	gtatcc	cggtgtgaa 1407	
Qy	1516	tcagttat	gtgttat	gtataa	aatatga	agcaac	ctttag	agat 1558		
Db	1408	tcagctac	gtgtgt	ctacga	aaaac	ctgaagat	catcc	ctgtgc	gt 1450	
RESULT 7										
AAZ61789										
ID	AAZ61789 standard; cDNA; 1816 BP.									
XX	AAZ61789;									
AC	AAZ61789;									
XX	27-MAR-2000 (first entry)									
DT	27-MAR-2000 (first entry)									
XX	cDNA encoding murine ADP/ATP transporter family protein, SEQ ID NO:262									
DE	cDNA encoding murine ADP/ATP transporter family protein, SEQ ID NO:262									
KW	Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;									
KW	embryonic skin cell; keratinocyte stem cell; transit amplifying cell;									
KW	secreted; transmembrane; inflammation;									

KW anglogenesis; tumour vascularisation; growth disorder;
 KW developmental disorder; skin wound; hair follicle disorder;
 KW anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.
 OS Mus sp.
 XX WO955865-A1.
 XX
 XX
 XX 04-NOV-1999.
 XX
 XX 29-APR-1999; 99WO-NZ00051.
 XX
 XX 29-APR-1998; 98US-0069726.
 PR 09-NOV-1998; 98US-0188930.
 XX
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 XX
 PI Strachan L, Sleeman M, Watson JD, Onrust R, Kumble A, Murison JG;
 DR WPI: 2000-072177/06.
 XX P-PSDB: AAY76084.
 XX
 PF Novel polynucleotides useful for the treatment of various conditions
 PT including wounds and cancer -
 XX
 XX PS Claim 1; Page 162; 235pp; English.
 XX
 CC The invention relates to novel nucleic acid sequences derived from rat
 CC dermal papilla, human keratinocytes and neonatal foreskin fibroblasts,
 CC and mouse embryonic skin, keratinocyte stem cells and transit amplifying
 CC cells. Polypeptides of the invention may be used to treat inflammation,
 CC cancer and neurological diseases. The proteins may be used to stimulate
 CC the growth and motility of keratinocytes, to inhibit the growth of
 CC cancer cells, to modulate angiogenesis and tumour vascularisation, to
 CC modulate skin inflammation, to modulate epithelial cell growth and to
 CC inhibit binding of HIV-1 to leukocytes. The invention may also be used
 CC to treat growth and developmental defects, skin wounds and hair follicle
 CC disorders. Sequences AAZ61606-261832 represent cDNA sequences derived
 CC from several mouse, rat or human skin cell types. Sequences
 CC AAZ61606-261649, AAZ61725-261765, AAZ61802-261811 and AAZ61826 encode
 CC proteins with an N-terminal signal sequence, indicating that the proteins
 CC are secreted. Sequences AAZ61650-261668, AAZ61766-261780, AAZ61812-261817
 CC and AAZ61827-261829 encode proteins with one or more putative
 CC transmembrane domains.
 CC
 XX
 XX Sequence 1816 BP; 421 A; 475 C; 537 G; 383 T; 0 other;
 SQ

Query Match 20.4%; Score 545.4; DB 21; Length 1816;
 Best Local Similarity 64.9%; Pred. No. 1.4e-112;
 Matches 807; Conservative 0; Mismatches 436; Indels 0; Gaps 0;

QY 316 agggagaaattttactactcggagatgcaacaagaatgggaagctgatttgaagaat 375
 Db 216 agcgagaaattgtgcaagcaggtgcaagaaccttgatgagcaactgacttgaagaat 275
 QY 376 ttatgaagttacctaagaagacaggaagaagaatgaatggcatttaagaagttaaca 435
 Db 276 ttgtacttccctccaagatcagagaaacaaacgagagctggttcaagaagcttgaca 335
 QY 436 aaataatgtatgaaataatgtaggctcagaatgtcgcctctccagacactggtc 495
 Db 336 aaagaatgtgtcgaatcagatgctcagagatcagatcagcgtccctcggagactggtg 395
 QY 496 tgactattctgaacaacagcagagttgattcttcaagaatgatgtatgtgagaca 555
 Db 396 tcaagatctcgaacagcagcgagagaagtcttaagaagcagatgaagaatgacaga 455
 QY 556 tgcacagtgcagctgaatgaatgagacactcttatttaaccctgtaacagactgt 615
 Db 456 tgcacatgcagctggaagagtgaggaactacacacccctgcgacccctgtgagagaatcc 515
 QY 616 aggaatattatcgtttctggaacatctacagaatgtgacatagggagacttaacta 675

Db 516 cggagatactcctgtactcggagcactgcacatcttctgattcgtgtgagatccgacag 575
 QY 676 ttccagatgaattcaccggaagacgaaaaaaaatccggacaatggtggtggagcgtttgg 735
 Db 576 ttccagatgaattcaccggaagacgaaaaaaaatccggacaatggtggtggagcgtttgg 635
 QY 736 caggagcattgtgtgtgtctctcgaacaagaacactgcctcttgacccgtctgaata 795
 Db 636 caggaggtggtggtggtggt 695
 QY 796 tcatgtatcaggttccaggttccaaatcagacaataatgaacatatgtgtgtgtgtgtgt 855
 Db 696 tcatgtatcaggttccaggttccaaatcagacaataatgaacatatgtgtgtgtgtgtgt 755
 QY 856 agatgttaagaagagagatccgtcgtcttggagggaggaatgtgtaacaagcttcatca 915
 Db 756 agatgtatcagagagggagggagggagggagggagggagggagggagggagggagggag 815
 QY 916 aaattgtcctcgaagacagctgttaattcttggacatagacaagtlacagaagtactta 975
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 QY 976 ctgaagaagacaaaataatgaacatttgagagatttattctgttccatggtgtgag 1035
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 QY 1036 caactgcacagacttttatatccatgtgaggttatgaagaacagcgtgtgtgagca 1095
 Db 936 ccattgcccagaagtagcatctaccacaaatgaggggttcgaagaacccgaatgtccctgcga 995
 QY 1096 aaactgagcagctactcgtgaatatatgattgtgcgaagaagatttgaacatgaagct 1155
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 Db 1116 tgcgactagcgtctatgagacatltgaaataactgtgtccgcgcgttaacgagtaaca 1175
 QY 1276 ctgtaaacccctgagatcgt 1335
 Db 1176 gtgcagaccccggt 1235
 QY 1336 agctggcagcagctaccatcttggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1395
 Db 1236 agctggcagcagctaccatcttggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1295
 QY 1396 aaggttccccaacagctgaatatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1455
 Db 1296 agggcagcagctgt 1355
 QY 1456 taccaggaacttacaagaagcgtacaccccaactcatgaaggtgtgtgtgtgtgtgtgt 1515
 Db 1356 ccttggcgtctacagggggt 1415
 QY 1516 tcaagttaatgt 1558
 Db 1416 tcaagtaatgt 1458

RESULT 8
 AAC97722
 ID AAC97722 standard; cDNA: 1816 BP.
 XX AAC97722;
 AC
 XX
 DT 08-MAR-2001 (first entry)
 XX
 DE Skin cell cDNA, SEQ ID NO: 262.

XX	Mouse; skin cell; cyostatic; antiinflammatory; anti-HIV;
KW	nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine;
KV	keratinocyte growth stimulation; cancer; angiogenesis inhibition;
KW	inflammation; neurological disease; ss.
XX	
OS	Mus sp.
XX	
PN	MO200069884-A2.
PD	23-NOV-2000.
XX	
PF	15-MAY-2000; 2000WO-NZ00075.
XX	
PR	14-MAY-1999; 99US-0312283.
XX	
PA	(GENE-) GENESIS RES & DEV CORP LTD.
PI	Watson JD, Strachan L, Onrust R, Sleeman M, Kumble KD, Murison JG;
XX	
DR	WPI: 2001-007495/01.
DR	P-PSDB: AAB55958.
XX	
PT	New isolated polynucleotide used in the identification of genetic
PT	disorders and encoding polypeptides used for treating inflammatory
PT	disease, cancer and neurological diseases -
XX	
PS	Claim 1; Page 223-224; 352pp; English.
XX	
CC	The present polynucleotide encodes a polypeptide which is expressed in
CC	mammalian skin cells. The polypeptide is useful for stimulating
CC	keratinocyte growth and motility, inhibiting the growth of cancer cells,
CC	modulating angiogenesis, inhibiting angiogenesis and vascularisation of
CC	tumours, modulating skin inflammation, stimulating the growth of
CC	epithelial cells, inhibiting the binding of human immunodeficiency virus
CC	(HIV)-1 to leukocytes, and treating inflammatory disease, cancer and
CC	neurological diseases. The polynucleotide can be used as a marker, in
CC	the identification of genetic disorders, and for the design of
CC	oligonucleotides for examining expression patterns.
XX	
SQ	Sequence 1816 BP; 421 A; 475 C; 537 G; 383 T; 0 other:

Query Match	20.44;	Score 545.4;	DB 22;	Length 1816;
Best Local Similarity	64.9%;	Pred. No. 1.4e-112;		
Matches 807;	Conservative 0;	Mismatches 436;	Indels 0;	Gaps 0;

Db	316	aggagaaaatttctactctgagatgcaacaaagatgggaagctggaatttgaagaat	375
Db	216	agcgaagaattgtgcaagcagtgacaaagccttgatgggcaactggacatttgaaggt	275
QY	376	ttatgaagttaccttaaaaccatggaagaataatgaattgacatttaagtttagaca	435
Db	276	ttgtacattacctccaagatcatcaggaaaaaactgtaggctgggttcaagagttcggaca	335
QY	436	aaaataatgatcgaaaaaattgagcttcaagaattgtccagtcctccagacaactgggtc	495
Db	336	aaaagaatgatggctcgaatcgatgctcaaggatgatcatgacgacctggggacccgggtg	395
QY	496	tgaattcttgcgaacaaacagcagatgtgatcttcaagaactgaaatgatttgatggaca	555
Db	396	tcaagatctcggaaacagcagcaggaagaatcttcaaaagacatgataagaatgacacga	455
QY	556	tgcagtgtagctggaatgaatgagagagactcttcttaactcccttcaagaactg	615
Db	456	tgaacctatcattggaagaagctggaaggactccacctcccttgcaacctgttgagaacatcc	515
QY	616	aggaatatccggttctcggaaacatttcaagaagatgacataagggaatagacttaacta	675
Db	516	cggagatcatcctcgtacggaagcactcgacgatcttgcattgctggtgagaaatccgaacg	575
	676	ttccagatgaattcaacggaagaacgaanaaatccggacaatggttggaagcagcttttg	735

Db	576	lccacgaatgaattccacagctggaaggagagcagacgaggagatgctgctgtagaggaacccctgtgtg	635
Qy	736	caggagagcatgtcgtgtgtgtctctctcctgaaacagacactgcccccttctgagacccgtctgtaaa	795
Db	636	caggagagtgaggagcaggaggacagtttccagaaacctgcagacatgcacccccctggagcagactgaag	695
Qy	736	tcaatgacaggtcttccacggttccaataatcatgacacaataatgaaacataattgtgtgtcttcgac	855
Db	636	tgtcatatgcagttccatctgctccctccgcagacaacaatgtgcatctgaagtgtgattctcaac	755
Qy	856	agatgtgtaaagaagagggagatccgcctgtttggaggggaaatgtgtataaacgtcatca	915
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Db	816	aaatgtccccctgagttcggccatccaattctcatgtgacatgtgacagatgaaacggtcttgctg	875
Qy	976	ctgaaagaagacaacaaaatagaaacatttgagagattattctctgttccatctgactgagag	1035
Db	876	gtatgagatcagagagacgctgtgagatccacagaaagctgtgtgacaggtcctcttgcccgag	935
Qy	1036	caactgcacacactttatatatccaatgtgaagttatgaaacacagcgtgcgtctgtagca	1095
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Qy	1096	aaactgggcagatctctggaatatatattgtgtccaaagaagactttgtgaacatgaagct	1155
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Qy	1156	tggagagcttlttacaagaagcctatgttcccaattatagttacatccatgacattagca	1215
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Qy	1216	tagatctgtcgtgtatgagctcctctggaagcccatatgtgcctgtgacataatttgcacaaagatt	1275
Db	1116	tcgacctagctgtctatgagagacattggaataacccgtgtccagcgtctagcagatgaaaca	1175
Qy	1276	ctgtaaacccctggagcatatgtgtgtcttgagatgctgtgcctatccacacctgtgtgc	1335
Db	1176	gttcagagacccgggtgtgtctgtgtcctctgtgcctgtgtgtactatctccagtactgtgtgc	1235
Qy	1336	agcttggccagcttaccatctgtgcttgtgtgaaactcgtcatctgacagcgtcttcaagcatgttag	1395
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Qy	1396	aaggttccccacagctgaatatgtgtgtgctctcttcgcagcaattatttccaaagaagaa	1455
Db	1296	agggcgcacactgtgaatcacatgtagcagcctcttccaacagaatctctgtcgagactgtgggg	1355
Qy	1456	taccagagactttaaaggagcatccaccccaacttcatgaagtggtccctgtctgtagca	1515
Db	1356	cccttgggctcttaccggggggtcgtgcccccaacttcatgaagtgagatccccgctgtgtgagca	1415
Qy	1516	tcaattatgtgttcatgaaatatgaagaacaaactttagagatt	1558
Db	1416	tcagctagctgtgtctacgaaaaactgtgaatccctctgggctt	1458
RESULT 9			
AAZ65058			
ID	AAZ65058	standard; cDNA; 3333 BP.	
NC	AAZ65058;		
XX	05-APR-2000	(first entry)	
DT	Membrane-bound protein PRO1106 encoding cDNA.		
DE	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand.		
KM	pharmaceutical; receptor immunoadhesin; gene mapping; ss.		
XX	Homo sapiens.		

XX W09963088-A2.
XX
XX 09-DEC-1999.
XX
PF 02-JUN-1999; 99WO-US12252.
XX
PR 02-JUN-1998; 98US-0087607.
PR 02-JUN-1998; 98US-0087609.
PR 02-JUN-1998; 98US-0087759.
PR 03-JUN-1998; 98US-0087827.
PR 04-JUN-1998; 98US-0088021.
PR 04-JUN-1998; 98US-0088025.
PR 04-JUN-1998; 98US-0088028.
PR 04-JUN-1998; 98US-0088029.
PR 04-JUN-1998; 98US-0088030.
PR 04-JUN-1998; 98US-0088033.
PR 04-JUN-1998; 98US-0088126.
PR 05-JUN-1998; 98US-0088167.
PR 05-JUN-1998; 98US-0088202.
PR 05-JUN-1998; 98US-0088212.
PR 05-JUN-1998; 98US-0088217.
PR 09-JUN-1998; 98US-0088655.
PR 10-JUN-1998; 98US-0088722.
PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088824.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 11-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
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PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
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PR 17-JUN-1998; 98US-0089539.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 22-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.

PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.
PR 20-JUL-1998; 98US-0093339.
PR 30-JUL-1998; 98US-0094651.
PR 04-AUG-1998; 98US-0095282.
PR 04-AUG-1998; 98US-0095285.
PR 04-AUG-1998; 98US-0095301.
PR 04-AUG-1998; 98US-0095302.
PR 04-AUG-1998; 98US-0095318.
PR 04-AUG-1998; 98US-0095321.
PR 04-AUG-1998; 98US-0095325.
PR 10-AUG-1998; 98US-0095916.
PR 10-AUG-1998; 98US-0095929.
PR 10-AUG-1998; 98US-0096012.
PR 11-AUG-1998; 98US-0096143.
PR 11-AUG-1998; 98US-0096146.
PR 12-AUG-1998; 98US-0096329.
PR 17-AUG-1998; 98US-0096757.
PR 17-AUG-1998; 98US-0096756.
PR 17-AUG-1998; 98US-0096758.
PR 17-AUG-1998; 98US-0096773.
PR 17-AUG-1998; 98US-0096791.
PR 17-AUG-1998; 98US-0096867.
PR 17-AUG-1998; 98US-0096891.
PR 17-AUG-1998; 98US-0096894.
PR 17-AUG-1998; 98US-0096895.
PR 17-AUG-1998; 98US-0096897.
PR 18-AUG-1998; 98US-0096949.
PR 18-AUG-1998; 98US-0096950.
PR 18-AUG-1998; 98US-0096959.
PR 18-AUG-1998; 98US-0096960.
PR 18-AUG-1998; 98US-0097022.
PR 19-AUG-1998; 98US-0097141.
PR 20-AUG-1998; 98US-0097218.
PR 24-AUG-1998; 98US-0097661.
PR 26-AUG-1998; 98US-0097951.
PR 26-AUG-1998; 98US-0097952.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097954.
PR 26-AUG-1998; 98US-0097955.
PR 26-AUG-1998; 98US-0097971.
PR 26-AUG-1998; 98US-0097974.
PR 26-AUG-1998; 98US-0097978.
PR 26-AUG-1998; 98US-0097979.
PR 26-AUG-1998; 98US-0097996.
PR 26-AUG-1998; 98US-0098014.
PR 31-AUG-1998; 98US-0098525.
PR 16-SEP-1998; 98US-01100634.
PR 12-JAN-1999; 99US-0115565.
XX
XX
XX (GETH) GENENTECH INC.
XX

PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 28-JUL-1999; 99US-0146232.
PR 17-AUG-1999; 99US-0149386.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.

(GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gertsen ME, Goddard A, Godowski PJ,
PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF,
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT;
PI Zhang Z;

DR WPI: 2001-032160/04.
P-PSDB; AAB65241.

PT PRO polynucleotides used to produce polypeptides used to target
PT bioactive molecules such as toxins, radiolabels or antibodies, to
PT specific cells, to cause targeted cell death -

XX PS Claim 2; Fig 205; 935pp; English.

CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
CC can be used for targeted delivery of bioactive molecules, such as
CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA
CC and DNA. They may also be used to produce transgenic animals which are
CC used to develop and screen therapeutically useful reagents. The PRO
CC nucleotide and protein sequence can be used for tissue typing and in
CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
CC sequences given in the exemplification of the present invention.

XX Sequence 3334 BP; 788 A; 848 C; 983 G; 715 T; 0 other;

Query Match 20.3%; Score 543.8; DB 22; Length 3334;
Best Local Similarity 64.8%; Pred. NO. 4.1e-112;
Matches 806; Conservative 0; Mismatches 437; Indels 0; Gaps 0;

OY 316 agggagaaatttactctgagatgcaacaagaatgggaagctgatttgaagat 375
DB 215 agcagaaattgtacaagctggaagtaagaagccttgaggcagctacttgaagat 274
OY 376 ttatgaacttaagaacatgagaagaatgaatgtgcatltagaagttagaca 435
DB 275 ttgtccatcatcocaagatcatgagaagaagctgagtgctgtttagaatttgaca 334
OY 436 aaaaatgatgaaaatgagcttcaagaatgtccagctctccagacacttggtc 495
DB 335 aaaagaatgatgacgcatgtgacgcgcagagatcatgcatcccttgaggacttggag 394

OY 496 tgactattctgaacaacagcagagttgattcttcaagaacatgatgttgaagaca 555
DB 395 tcaagatatctgaacagcagcagagaaaaattctcaagagctgataaaacggcaca 454
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DB 995 agacagcgcagactcagaaatgctgactggtccagagaggtccctgscagagaagg 1054
OY 1156 tggagcttcttaacaagctatgttcccaattattagatatactatctatgacga 1215
DB 1055 tggccgcttctcaaaagctatgtcccaacatgtcggcatcatccctatgcccga 1114
OY 1216 tagactctgtgtatgagctcttgaagctcctatgtgctgataatttgaagaagat 1275
DB 1115 tgcagcttgcagctcagagaagcgtcaagaatgctgctgacagacatctgagfaga 1174
OY 1276 ctgtaaaccttgagctcatgtgtctgtgagatgctgtcttaccagacgtgtgtc 1335
DB 1175 ggcgcgaccocggcgtgtgtgtgtcctgctggtgcacatgctccagctatctgtgc 1234
OY 1336 agcttgccagctaccatctgtgtgtgtgagacgtcgcgtacgtcaagctcaagctgtg 1395
DB 1235 agcttgccagctaccatctgtgtgtgtgagacgtcgcgtacgtcaagctcaagctgtg 1294
OY 1396 aaggtccccaagctgatatggtgtgtgctcttcgcagaaatttcccaagaagaa 1455
DB 1295 agggcgctccggaggtgacatgagcagccttcaaacatctctgtcgagccggagg 1354
OY 1456 taccaggaacttaccagagcatcaccacaaactcatgaagggtgctccctgtatgaa 1515
DB 1355 ccttcgggctgtacagggggtcgtgcccacactcatgaaggtcatcccaagtgtgagca 1414
OY 1516 tcaatgattgtgttataatgaatgaagcaactttaggaat 1558
DB 1415 tcaatgattgtgttataatgaatgaagcaactttaggaat 1457

RESULT 12
AAK53194
ID AAK53194 standard; cDNA; 549 BP.
XX
XX AAK53194;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 2723.
DE
XX
XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
XX Homo sapiens.
OS
XX
XX MO200157190-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 05-FEB-2001; 2001MO-US04098.
PF
XX
XX 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RF, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R.
XX
XX WPI; 2001-476283/51.
DR P-PSDB; AAM80061.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
XX Claim 1; Page 4947; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine; cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
XX Sequence 549 BP; 146 A; 122 C; 152 G; 129 T; 0 other;
SQ

Query Match 20.2%; Score 540.2; DB 22; Length 549;
Best Local Similarity 99.4%; Pred. No. 1.2e-111;
Matches 542; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 86 gccctcgatctccgctgactctcctcgccagcgccgctcgctcgctctggaaccatgttgcg 145
+ |||||
Db 5 gtctcgatctccgctgactctcctcgccagcgccgctcgctcgctctggaaccatgttgcg 64

QY 146 ctgctcgcgaggaactcgctgctgcccacgcgcgctgctgccaagaagcgagacgcgaagcg 205

Db 65 |||||
ctgctcgcgaggaactcgctgctgcccacgcgcgctgctgccaagaagcgagacgcgaagcg 124
QY 206 ctacgagaccctcttccagcactggaaccgcaatgggagcagtggtgagacatcgcca 265
+ |||||
Db 125 ctacgagaccctcttccagcactggaaccgcaatgggagcagtggtgagacatcgcca 184
QY 266 gctgcaggaagggtcaggaacctgggcatccctctgggccaagacgcgagagaanaat 325
+ |||||
Db 185 gctgcaggaagggtcaggaacctgggcatccctctgggccaagacgcgagagaanaat 244
QY 326 ttctactcgtgagatgtaacaaatgggaagctggatttgaagaattttgaagta 385
+ |||||
Db 245 ttctactcgtgagatgtaacaaatgggaagctggatttgaagaattttgaagta 304
QY 386 ccttaagaccatgataagaanaatggaattgcatcttaagaagtttgaacaaataatga 445
+ |||||
Db 305 ccttaagaccatgataagaanaatggaattgcatcttaagaagtttgaacaaataatga 364
QY 446 tggaaaattgaggtctcagaanaatgltccagctctccagacacgtggtctgactttc 505
+ |||||
Db 365 tggaaaattgaggtctcagaanaatgltccagctctccagacacgtggtctgactttc 424
QY 506 tgaacacaagcagagttgattcttcaagcatgtgattgtagggacaatgacatgga 565
+ |||||
Db 425 tgaacacaagcagagttgattcttcaagcatgtgattgtagggacaatgacatgga 484
QY 566 ctggaatgaatgagagactactcttatttaacctgttacagacatgagaaattat 625
+ |||||
Db 485 ctggaatgaatgagagactactcttatttaacctgtgttacagacatgagaaattat 544
QY 626 ccgctt 630
+ |||||
Db 545 ccgctt 549

RESULT 13
AAS44597
ID AAS44597 standard; DNA; 2625 BP.
XX
XX AAS44597;
AC
XX
XX 18-DEC-2001 (first entry)
DT
XX
XX Human full-length polynucleotide sequence #22.
DE
XX
XX Mammal: human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukaemia;
KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
KW nervous system disorder; inflammatory disorder; cell differentiation; ds;
KW anglogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;
KW cytostatic; antipneumatic; antiarthritic; vulnery; antiinflammatory;
KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
KW neuroprotective; osteopathic; antidiabetic; antiashmatic; antiallergic;
KW immunostimulant; analgesic; gene therapy.
XX
XX Homo sapiens.
OS
XX
XX MO200164834-A2.
PN
XX
XX 07-SEP-2001.
PD
XX
XX 26-FEB-2001; 2001MO-US04926.
PF
XX
XX 28-FEB-2000; 2000US-0515126.
PR 18-MAY-2000; 2000US-0577409.
PR 17-JUN-2000; 2000US-0597707.
PR 14-JUL-2000; 2000US-0616807.
PR 19-SEP-2000; 2000US-0664641.
XX
XX (HYSE-) HYSEQ INC.

XX 18-DEC-2001 (first entry)
XX
DE Human contig polynucleotide sequence #22.
XX
KW Mammal; human; rhesus monkey; baker's yeast; fission yeast; Norway rat;
KW mouse; Chinese hamster; African clawed frog; fruit fly; dog; leukemia;
KW cancer; lymphoma; neuroblastoma; autoimmune disorder; cell proliferation;
KW nervous system disorder; inflammatory disorder; cell differentiation; ds;
KW angiogenesis; stem cell growth factor; activin; inhibin; cartilage; burn;
KW genetic disorder; bone regeneration; tendon; ligament; tissue repair;
KW cytoskeletal; antirheumatic; antiarthritic; vulnery; antiinflammatory;
KW antibacterial; immunosuppressive; vasotropic; antiparkinsonian;
KW neuroprotective; osteopathic; antidiabetic; antisthmatic; antiasthmatic;
KW immunostimulant; analgesic; gene therapy.
XX
OS Homo sapiens.
XX Synthetic.
XX
PN WO200164834-A2.
XX
XX 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04926.
XX
XX 28-FEB-2000; 2000US-0515126.
XX 18-MAY-2000; 2000US-0577409.
XX 17-JUN-2000; 2000US-0597707.
XX 14-JUL-2000; 2000US-0616807.
XX 19-SEP-2000; 2000US-0664641.
XX
PA (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Wehrman T, Wang J, Ma Y, Wang D, Chen R, Xu C;
PI Dmanac R;
XX
XX WPI: 2001-589862/66.
XX P-PSDB: AAU27869.
XX
XX Novel polypeptides and nucleic acids obtained from cDNA libraries
XX prepared from various human tissues, for diagnosis, treatment of
XX cancer, neurological, inflammatory disorders and for use in arrays for
XX detection -
XX
XX Claim 1; SEQ ID NO 366; 153bp; English.
XX
XX Sequences AAS44576-AAS44919 represent full-length polynucleotides and
XX contig polynucleotides encoding polypeptides of the invention. The DNA
XX and protein sequences are useful for the treatment, diagnosis and
XX prevention of various types of disorder in a mammalian subject such as a
XX human, dog, monkey, mouse, hamster or rat. The disorders include cancers
XX such as leukemia, lymphoma and neuroblastoma, autoimmune disorders such
XX as multiple sclerosis, connective tissue disease, rheumatoid arthritis,
XX diabetes mellitus, allergic rhinitis, asthma and eczema, nervous system
XX disorders such as Parkinson's disease, Alzheimer's disease, Huntington's
XX chorea, amyotrophic lateral sclerosis, spinal muscular atrophy and
XX Wernicke disease, inflammatory disorders such as nephritis, Crohn's
XX disease, ischemia-reperfusion injury, shock, sepsis and inflammatory
XX bowel disease. The sequences exhibit activity relating to angiogenesis,
XX cell proliferation, cell differentiation, stem cell growth factor,
XX activin or inhibin. Therefore, they can be used to manipulate stem cells
XX in culture to give rise to neuroepithelial cells that can be used to
XX augment or replace cells damaged by illness, accidental damage or genetic
XX disorders. The sequences may also be used for regeneration of bone,
XX cartilage, tendons and ligaments and in tissue repair and burn healing.
XX Note: Some sequences for this patent did not form part of the printed
XX specification, but were obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 2644 BP; 568 A; 825 C; 743 G; 508 T; 0 other;

Query Match		20.0%;	Score 534.2;	DB 22;	Length 2644;
Best Local Similarity		61.9%;	Pred. No. 5.4e-110;		
Matches 864;		Conservative 0;	Mismatches 528;	Indels 3;	Gaps 1;
Oy	186	gacgcgagcagccgacgcgacgtacagacccctctccagcagcctgcagccgacatgggagac	245		
Db	133	gaccgcgagcggcgccgacgctgctgcctctgtctcgaaggcgctcgacagtaaacagaat	192		
Oy	246	ggaagtgtgacacatcgcgagctgcagaggagggctcaggaacctgggc--atccctctg	302		
Db	193	ggccgctggagcgcgacagagctgcgcagggcgctggcagcctggcgcggggcaaccca	252		
Oy	303	ggccagagcgcggcgaggaaattttactcttgagatgcacacaagaatgggaagctg	362		
Db	253	gaccccgcgcccaacaggtatctctctgagggtgatgtgcacccaagatggcgggctc	312		
Oy	363	gatttgaagaattatgaattacctaagaacacatgagaagaatgtgacatt	422		
Db	313	gacctggaggaatttcccgctatctgcagagcggaacscgctcgtctgctcatgtt	372		
Oy	423	aagagtttagacaaataatgatgaaataatgaagcttcagaataatgtccatcttc	482		
Db	373	cacagcttgacccggaaccagatggtacacatgactgtctctgagatccacaagaatttc	432		
Oy	483	cagacactgggtctgactatttctgaaacaaacagacagatgtattcttcaaaagatgat	542		
Db	433	cgagctcgggcatcttcacatctcgtgagcagggctggagaataattgtcacagatggac	492		
Oy	543	gttatggagacatgacacgtgactgagatgaatgcagagacactcttacttaattcct	602		
Db	493	cgagacgycacaatgaccatgtgactgcagaataaggcgcgacactctctgttgcattcg	552		
Oy	603	gtacagacatttgagaaatataccgttctcgtgaaacattctacagaatgtacatggg	662		
Db	553	ctggaataatgaggagacgtgtgattctctggaagcattccacgltctcgtacattggc	612		
Oy	663	gatagcttaactatccagatgaaatcccggaagaacggaataatccggacatgtgtgg	722		
Db	613	gagtgcctgacagtgccgagcagatctccaaagcaagaagagctgcagggacatgtgtgg	672		
Oy	723	agcgacgttctggcagagggcagctgtgtgtctctctcgaacaacgacgctccctctg	782		
Db	673	aaacgctggtggccggcgagtgccaggtgctgtcgtgtaacgagacggagccctctg	732		
Oy	783	gaccgtctgaataatcatgatgacaggttcaacggttcaaaatcagacaaatgaacatat	842		
Db	733	gaccgctccaaaggtcttcatgacgttccatgcttcaaaagacaaacggctgaacatcct	792		
Oy	843	gttgcttgcacagatgtgaaagaaggaggtatccgctcgtcttgaggggaaatggt	902		
Db	793	ggggggtctcgaagcatggtctcttgaggaggacatccgctcctctgtggcgcgaaatggt	852		
Oy	903	acaacgcatcaaaatgtctctctgagacagctgtttaaattctggtcatatgacagatc	962		
Db	853	attaatgtaccacaagatgtgcccccgagtcagctatacgaattcatgtcctatgacagctc	912		
Oy	963	aagaatgaactactgaagaagagacaataataggacaatttgagagatattatctggt	1022		
Db	913	aagagggcaccctctgggagcagcagagacactgcatgtgcagggcgcttctgtgtgctgc	972		
Oy	1023	tcacatgcttgagaacacgcagcagcacttttatatccatggggggtatgaaacccgg	1082		
Db	973	tcacctgtgtgtgcacacggcccaacacatcatcttaaccttgaagggtgtcgaagaacggg	1032		
Oy	1083	ctggcttgaggcaaaactggtgcagctactctggaatatatgattgtgcgaagaagaatttg	1142		
Db	1033	ctgacctggcgccggagcggcgacgataaagggtcgtgcgtcgcgcagggcgatcctgt	1092		
Oy	1143	aaacatgaagcctgtggagctttttacaagaagctatgttcccaatttatgtgatacta	1202		
Db	1093	gagagggagggcccccgtctcttaccgcggtacacccccaacgctgtctgggacatc	1152		
Oy	1203	ccattagaggcatagatctgtctgtgtatgagctcttgaagctcttatgtgtgataat	1262		

Db	1153	ccctatgctggagacacacgaccttgcgcgtctacgagaccttgaaagacttggcttccagcag	1212
Qy	1263	tttgcaaaaagattctgtttaaacccttgaggtcattggttctgagtgatgcgttcttacc	1322
Db	1213	tacagccagactcgcgcagaccacagacatctctgtctcctgcctgcctgcgttaccatactc	1272
Qy	1323	agcaacctgtgttcagctcgcgcagcttaccacattggtcttctgtgtgaagactgcattgcgct	1362
Db	1273	agcactctgcgcgcagataagacagattaccgcttgcgccttgcgtccgcagccgattcagggca	1332
Qy	1383	caagccatgttagaaggtctccccaacagctgatatgtgttgctgcctcttcgacgacattatt	1442
Db	1333	caagctctccatccaggggtggtgcccccaagctgtccatgctcgtctggtctgcatacctctg	1392
Qy	1443	tccaaaagaagataccaggaacttcaagaggcatcaccccaactcatgtaaagtgtctc	1502
Db	1393	tcccaggaggtgacatgcgtgcgggctcttaccggtggtatcgcccccaacttcatgaagtatt	1452
Qy	1503	ctctctgtagcagcatcagttatgtgtttatataaatttgaaagcaaaatttagaggtacc	1562
Db	1453	ccagctgtgagacatctcctctatgtgttcttagaagaacatgaagcagcctcttgggtaccg	1512
Qy	1563	cagaatgatgttgc 1577	
Db	1513	tccagatctctctgc 1527	
RESULT 15			
XX	AACT6538		
XX	AACT6538	standard; cDNA; 1481 BP.	
AC	AACT6538:		
XX			
DT	08-FEB-2001	(first entry)	
XX			
DE	Human ORFX ORF2093 polynucleotide sequence SEQ ID NO:4185.		
KW	Human: open reading frame; ORFX; detection; cytosolic; hepatotropic;		
KW	vulnary; antipsoriatic; antiparkinsonian; neurotropic; neuroprotective;		
KW	anticonvulsant; osteopathic; antiarthritis; immunosuppressant; cardiant;		
KW	immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;		
KW	hypotensive; dermatological; immunosuppressive; antiinflammatory;		
KW	antiviral; antibacterial; antifungal; antirheumatic; antithyroid;		
KW	antianaemic; gene therapy; cancer; proliferative disorder; hypertension;		
KW	neurodegenerative disorder; osteoarthritis; graft vs host disease;		
KW	cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;		
KW	cholesterol ester storage; systemic lupus erythematosus; infection;		
KW	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;		
KW	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;		
KW	bone damage; cartilage damage; antiinflammatory disease; coagulation;		
KW	thrombosis; contraceptive; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	W0200058473-A2.		
XX			
PD	05-OCT-2000.		
XX			
PF	31-MAR-2000; 2000WO-US08621.		
XX			
PR	31-MAR-1999; 99US-0127607.		
PR	02-APR-1999; 99US-0127636.		
PR	05-APR-1999; 99US-0127728.		
PR	30-MAR-2000; 2000US-0540763.		
XX			
PA	(CURA-) CURAGEN CORP.		
XX			
PI	Shinkets RA, Ieach M;		
XX			
XX	WPI: 2000-602362/57.		
OR	P-PSDB; AAB42329.		
XX			

PT	Novel nucleic acids and peptides derived from open reading frame X,
PT	useful for treating e.g. cancers, proliferative disorders,
PT	neurodegenerative disorders and cardiovascular disease -
PS	Claim 5; Page 3377-3378; 5507pp; English.
PS	
XX	
CC	AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC	which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC	sequences have activities such as: cytostatic; hepatotropic; vulnerary;
CC	antiproliferic; antiparkinsonian; nootropic; neuroprotective;
CC	osteoplastic; anticonvulsant; antiarthritic; immunosuppressant;
CC	immunostimulant; cardiac; thrombolytic; coagulant; vasotropic;
CC	antidiabetic; hypotensive; dermatological; immunosuppressive;
CC	antiinflammatory; antibacterial; antiviral, antifungal, antirheumatic;
CC	antihypoid; and antihaemic. The sequences can be used for determining
CC	the presence of or predisposition to, or preventing or treating
CC	pathological conditions associated with an ORFX-associated disorder. The
CC	nucleic acids can be used to express ORFX proteins in gene therapy
CC	vectors. The proteins and nucleic acids may be used to treat cancers,
CC	proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC	graft vs host disease, cardiovascular disease, diabetes mellitus,
CC	hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC	erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC	bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC	allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC	nocturnal haemoglobinuria, antiinflammatory disease: to enhance
CC	coagulation; to inhibit thrombosis; and as a contraceptive.
CC	
XX	
Sequence 1481 BP; 331 A; 411 C; 465 G; 273 T; 1 other;	
Query Match	18.5%; Score 494.4; DB 21; Length 1481;
Best Local Similarity	64.5%; Pred. No. 3.7e-101;
Matches 738; Conservative	0; Mismatches 406; Indels 0; Gaps 0;
QY	415 tggcatttaagaggtttagacaaaataatgatgatgaaaattgaggttcagaattgtcc 474
DB	2 tgggtgttaagagtttgacaaaagaatgatgatgagcattgacgcgagagatcatgc 61
QY	475 agtctctccagacactgtgtctgactatttctgacaaaagacagatgtgattcttaa 534
DB	62 agtccctcgcgactctggagatcagatatctgcgaacgacgacgaaaaattctcaaa 121
QY	535 gaattgatgtgatgggcaatgacacgacagtgacttgaaatgaaggagagactcttatt 594
DB	122 gcatgatataaaacgacgacgatgaccatcogactgtaagacagtgaggagactccactcc 181
QY	595 ttaatccgtttacagacatttgagaatattccgttcttggaacattctacagaattg 654
DB	182 tccaccocgttgaaaaacatcccgagatcatctctactctggaagattccacagattctg 241
QY	655 acataggagatgcttactactatccagatgaatttaacgaaagcagaaaaaattccggc 714
DB	242 atgtgggtgagagaattcaaaaggtcccgatgaaattcaacagtggaaaggacgcagcggga 301
QY	715 aatgttggaaggaaagcttttgcgagaggacattgctgtgtctgtctctcgacaagaactg 774
DB	302 tgtgttgagacactgtgtgcgagaggttggggcaggggccgtatccagaacctgcag 361
QY	775 ccccttggaccgcttctgaaaaatcatgatgcaggttccaggtttcaaatcagacaaatga 834
DB	362 ccccccgtgacaggtgtcaaggtgtccatgtgcaagtgccatgtcccgccagcaacaatttg 421
QY	835 acataattgtgtgctcttcgcacagatggttaaaaggagaggtatccgcctgcttgagg 894
DB	422 gcatcgtgtgtgtgtcttaactcagatgatctgagaagaaggggccagtgtaaccttggcgg 481
QY	895 gaatgtgtaacaagtcatacaaaattgctcctgtagacagctgttaaatcttgggcata 954
DB	482 gcaatgcatcaacgtctctcaaaattgtcccccgaatcagccatcaaatcattcagtcgt 541
QY	955 aacagtacaagaagtacttacttgaagaagacaaaataatagaaacatttgagagattta 1014


```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/945,283
; FILING DATE: 19920911
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ribando, Curtis P
; REGISTRATION NUMBER: 27976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 309-685-4011 ext. 513
; TELEFAX: 309-685-4128
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8438 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Pseudorabies virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 622..6495
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(1099, "g")
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(1267, "t")
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(1381, "c")
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(1566, "c")
; FEATURE:
; NAME/KEY: variation
; LOCATION: replace(7010, "g")
; ORGANISM:
; US-07-945-283-1

```

Query Match 1.8%; Score 48; DB 1; Length 8438;
Best Local Similarity 51.9%; Pred. No. 0.03;
Matches 108; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

```

QY 112 gccagccgcctcgtcctctggaccatgttgcgtcgtcgtcgggaacttcgcgctgccca 171
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4493 GCCACGGTCCGGGGCGACGAGGCGACAGAGTCGCGGCGCTGCTGCGCGCGGCGCG 4552
QY 172 ccgcgcctcgcagagcgagcgacgcgcgcctcgcagagcccttcctccagcgacatg 231
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4553 GCCCGGGGATGCGCTCGCGGAGCGCGAGCAGCGCGCGCTCACCCTCTCGAGGCGGG 4612
QY 232 accgcaatgggagcgagagtgtgtgacatcgcgcgcgtcgcagaggggtcaggaacctgg 291
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RESULT 15
US-08-998-416-186
Sequence 186, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter

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; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtung, Philipp
; APPLICANT: Reibschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPYII
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8589
; INFORMATION FOR SEQ ID NO: 186:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 615 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1074RP
; US-08-998-416-186

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Query Match 1.8%; Score 47; DB 4; Length 615;
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Search completed: August 18, 2002, 08:14:03
Job time: 17844 sec

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ACCESSION	BM460880							
VERSION	BM460880.1	GI:18509920						
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SOURCE	house mouse.							
ORGANISM	Mus musculus							
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AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.							
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JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .							
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)							
	Unpublished (1999)							
	Contact: Robert Strausberg, Ph.D.							
	Email: cgapbs-remail.nih.gov							
	Tissue Procurement: Aaron Hsueh							
	CDNA Library Preparation: Life Technologies, Inc.							
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	DNA Sequencing by: Agencourt Bioscience Corporation							
	Clone distribution: MGC clone distribution information can be							
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	http://image.lnl.gov							
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VERSION		AK015371.1	GI:12853684
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ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
AUTHORS		Carninci,P. and Hayashizaki,Y.	
JOURNAL		High-efficiency full-length cDNA cloning	
METHOD		Meth. Enzymol. 303, 19-44 (1999)	
REFERENCE		99279253	
AUTHORS		10349636	
2 (sites)			
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.			
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
Genome Res. 10 (10), 1617-1630 (2000)			
JOURNAL		20499374	
METHOD		11042159	
REFERENCE		3 (sites)	
AUTHORS		Shibata,K., Itoh,M., Atzawa,K., Nagao,K., Sasaki,N., Carninci,P., Kono,H., Akiyama,J., Nishi,K., Kitsuana,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsuno,T., Sakaguchi,S., Ikegami,T., Kasaiwagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,Y., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.	
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multiplexillary sequencer			
Genome Res. 10 (11), 1757-1771 (2000)			
JOURNAL		20530913	
METHOD		11076861	
REFERENCE		4 (sites)	
AUTHORS		The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	
Functional annotation of a full-length mouse cDNA collection			
Nature 409, 685-690 (2001)			
5 (bases 1 to 1674)			
Adachi,J., Atzawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Aizawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bulic,C., Carinci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hangack,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,D., Kojima,Y., Kono,H., Kouda,M., Koya,S., Kunikida,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Nunakura,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shigaawa,A., Shiraki,T., Soabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toyo,T., Yamamura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.			
Direct Submission			
Submitted (10-JUL-2000)			
Physical and Chemical Research (RIKEN), Laboratory for Genome			
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsunumi-ku, Yokohama			
kanagawa 230-0045, Japan (E-mail:genome-res@gsf.riken.go.jp,			

URL:<http://genome.gsc.riken.go.jp/>, Tel:81-45-503-9222,
Fax:81-45-503-9216)
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGACGAGAAGAGATCCAGACTCTTTTTCCTTTTTTTTAA 3'], cDNA was prepared by using triethanol thermo activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGACGAGATCGATTAAATTAATTAATGCCCCCCCCC 3']. cDNA was cleaved with BamH1 and XhoI. Vector: a modified pluviescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamH1. Host: DH10B.

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ORIGIN

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QY 1369 ctccgaatgagctcaagacatggttagaaggttccccaagcgaatattggttgctct 1428
DB 1309 CTGCGATGACAGGCTGTATGCTGGAAGG-----AAACAGTGCAGATGATGCACCTCA 1362

QY 1429 ttccagaaattattccaaagaagaataccaggaacttaccagaggcatcaccacaaact 1488
DB 1363 TTCAGAAATATATACACTAAAGAGGAAAGGAGATTTTTCAGGGGCTTCACCCCTAATG 1422
QY 1489 tcatgaagtgctccctgctgtgtagcagatgattgtgttatgataatgaagcaaa 1548
DB 1423 TCCCAAGCTCTTCCTGCGAGTGGGCGCATTCGCAAGTGTGCTCACAGACTAGTAAAGGC 1482
QY 1549 ctttagagtaaccagaatgatgtgca 1578
DB 1483 TTTTGGATTAACTAGAGTGAATACCA 1512

RESULT 5
BE731210 980 bp mRNA linear EST 15-SEP-2000
LOCUS 601567293F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842039 5',
DEFINITION mRNA sequence.
ACCESSION BE731210
VERSION BE731210.1 GI:10145202
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 980)
NIH-MGC http://imgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incycle Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.lnl.gov
Plate: LNCM534 row: j column: 24
High quality sequence stop: 676.
Location/Qualifiers
1. 980
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3842039"
/clone_lib="NIH_MGC_21"
/issue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

FEATURES
source
1. 980
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3842039"
/clone_lib="NIH_MGC_21"
/issue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: placenta; Vector: pORF7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 262 a 232 c 275 g 211 t
ORIGIN
Query Match 22.5%; Score 602; DB 10; Length 980;
Best Local Similarity 94.1%; Pred. No. 2.3e-91;
Matches 726; Conservative 0; Mismatches 30; Indels 16; Gaps 10;
QY 98 cgtgagcttctcggcgaagcgccgctgcttggagacatgttgctgctgagga 157
DB 6 CCGTGACTTCTCTGG-CAAGCGGCTGCGCTCTGGGACCATGTGCGCTGCGGGA 64
QY 158 ctccgagctgccacacgagcctgcgagagcgaggaacgacgacgctacagacct 217
DB 65 CTTCGTGCTGCCACCGCGGC--TGCAGGACGGGAGACACCGACGCGCTACAGACCT 122
QY 218 ctccagagcactgagccgaatgggaacgagatggtgagacatcgagcgtcagaagg 277
DB 1309 CTGCGATGACAGGCTGTATGCTGGAAGG-----AAACAGTGCAGATGATGCACCTCA 1362

Db	123	CTTCCAGGCACCTGGAACCGCAATGGGACGAGTGTGACATCGG-GAGCTGCAGAGGG	181
Qy	278	gtctgaagcaactgaggacatccctctgagcaggaagccgaggaagaatttactactg	337
Db	182	GCTCAGGAACCTGGGATCCTCTGTGGCCAGACGCCGAGGAGAAATTTTACTACTGG	241
Qy	338	agatgtcaacaaagatgaggaaagctgagttttgaagaattatgaagtlacctaaagacca	397
Db	242	ACATGTCAACAAAGATGGAGACGTGATTTTGAAGAATTTATGAGTACTCTTAAGACCA	301
Qy	398	tgaagaagaagaatggaattgcatcttaagaagtttagaacaagaataatgagaaaatlga	457
Db	302	TTAGAAGAACATGAATAATGGCATTTTAAAGATTAGACAAATAATGAATGAAAAATTGA	361
Qy	458	ggcttcagaagaattgtccagctctccacagacactggctgactatttcgaacaagaac	517
Db	362	GGCTTCAGAAATTTGTCCAGTCTCTCCAGACACTGGGTGACTATTTCGAAACAAACAGC	421
Qy	518	agaattgattcttcaaaagcatgattg-ttgatgagacaatgacagtgagctggaatgaat	576
Db	422	ACAGTTGATTTCTTCAAAAGCATGTGATGTTGATGGACATGACAGTGACACTGGAATGAAT	481
Qy	577	ggaagagactactcttatttaatactcgtttacagacacttgaagaagaattatccgtttctga	636
Db	482	GGAGAGACTACTCTTATTATTAATCCGTGTACAGACATTTAGGAAATTAATCCGTTCTGGA	541
Qy	637	aacattctcagaagaattgacatagaggaatagcttaactatccagaatgataccaagag	696
Db	542	AACATTCTACAGGA-TGACATATAGGGGATAGCTTAACCTTCCAGATGAAATTCACGGAAG	600
Qy	697	acgaaaaaaaatccgagacaatggtgagagcagcttttgacagaagcattgctggtgctg	756
Db	601	ACGAAAAAAATCCGACCAATGATGTGGAGGAGCAG--TTTGTGAGAGAGGAGATTG--TGGTGTG	657
Qy	757	tcttcgagaagaagcagctgccccttggagcc--gltcgaagaatcagatgagaggttcaag	813
Db	658	TTCTTGGAACAAGCACTGCCCTTGGACCCGTCTGAATAATTCATGATGAGGTT--CC	715
Qy	814	gttcaaatcagacaagaatgaacataatctgtgtgcttcgacagatggttaagaagaagag	873
Db	716	GGTCAACATCAGACACAACATGAACCTAAT--GGTGTCTCTGACAGATGATGCCCCGAGGG	773
Qy	874	gt 875	
Db	774	AT 775	
RESULT	6		
BE209622		839 bp mRNA linear EST 06-NOV-2000	
LOCUS	601874136F1 NIH_MGC_54 Homo sapiens CDNA clone IMAGE:4098849 5',		
DEFINITION	mRNA sequence.		
ACCESSION	BE209622		
VERSION	BE209622.1 GI:11103208		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	1 (bases 1 to 839)		
JOURNAL	NIH-MGC http://mgi.nci.nih.gov/ .		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-ri@mail.nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: CLONETECH Laboratories, Inc.		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	http://image.llnl.gov		
	Plate: L10M966 row: 9 column: 10		

FEATURES	High quality sequence stop: 610.	
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	/clone_lib="NIH_MGC_54"	
	/library_type="from chronic myelogenous leukemia"	
	/lab_host="DH10B (T1 phage-resistant)"	
	/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech); Site.1: SfiI (ggccgcctggcc); Site.2: SfiI (ggccatattgccc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGAGCC-3' and 3' adaptor sequence: 5'-ATCTAGAGCGCGGCGCATG-dr(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."	
BASE COUNT	243 a	150 c 140 g 306 t
ORIGIN		
Query Match	20.9%;	Score 558.6; DB 10; Length 839;
Best Local Similarity	92.8%;	Pred. No. 4.4e-84;
Matches	675; Conservative	0; Mismatches 39; Indels 13; Gaps 8;
Qy	1784 cacacaattatacttattcttctaataatccgcgaatctgcccgtgaatccgaaa	1843
Db	1 CACACAAATTAACTTATCTTCTTAAATACCTGCAAACTCTGCTCCGTGAATCCGAAA	60
Qy	1844 tctgaaaatgctactgctggaacaaatctgttctgtgtgtagagttataatcatlaa	1903
Db	61 TCTGAAATGTACTGCTGTTGAACAAATTTG- TTGTGTGTTAGATTATAATCATTTAA	119
Qy	1904 tcttaattcgggtggttaagttacgttcaagtccttaatatlaaatcttctgttta	1963
Db	120 TCTTTATTTTCGGGTGGTGTATACGTTTATGCAAGTCTCTTAATTAATTTCTTG- TTTA	178
Qy	1964 tatatttgaatgctttatagattctttaaattccctatagaacctaataagaana	2023
Db	179 TATATTGAATGCTTTTAATGATTTCTTAATTTCTTAATGAACATTAATTAAGAAA	238
Qy	2024 tcaatcattlaaatalacacttacagcaaaagcaccacaataagttatggttctatgct	2083
Db	239 TCATTACATTTAAATATATACCTTACAGCAAAAGCATCAATTAATGATGATGATGTC	298
Qy	2084 cttaattctcttcagctgtaatacgaatgaacacagtggtggaattctcgaagggaagtc	2143
Db	299 CTTATTTTCTTTCAGCTGAATACGAATGACACAGTGTGAATTTTGAAGGGAAATG	358
Qy	2144 atgaatatattattttagagtgaggaacttccaatcttaacacagcttacattattgt	2203
Db	359 ATGAATTAATTAATTTATTTAGTGGGACACTTTTCCATTTTACACATGTACCATTAATTTGGT	418
Qy	2204 tccctgagttatacactaatttcaglatatattactgttlaaatlaccaacacaaggaact	2263
Db	419 TCCGTGAGTTATACACTAATTTTCAGTATATTACTTTAAATTTACCAACACAGGCAATT	478
Qy	2264 ta-cttgaagaatccggttatactcgtgcaatgcttgaagaagcagcagaagaatt	2322
Db	479 TATTTTGAAGAAGATCCGTTTATCTGCGCA- TGCCTTGAAGAACAGAGGAAAGCAATCC	537
Qy	2323 tttagctgtatcagc-ttctcagagaagctttgttccttctgttcttctctac	2381
Db	538 TTGTGACTGATTAACGCTTCTGAGAGCAATCTTGTTCTCTT- GTCTTGTTCCTAC	595
Qy	2382 ctcttgaacacagatccggtt---agtcaagaagactcttgggacaattcttagtaac	2438
Db	596 CTTTGAATCAATTCGCCCTTTTAGTCAAGGAAGACTCTTGGAAGCACTTTTGTAGTAC	655
Qy	2439 ctgaattctcttctaattgcatgaagtgtatcatgaagcaagtgaatggtcttat	2498

QY	751	gtcgtctcttcgacaagcaagcaactgcgcctcttggaccgtctgaataatcatgtgtcagcttc	810
Db	242	GGCGCGTCTCTTAGAACAGACGACCGCTCCTTTGGATGCGCTCAAGGTCAATGACAGGTTCC	301
QY	811	acggttcaaaatcagacacaaatgaacatatttgtgtgtcttcgcacagaatggtlaaagaag	870
Db	302	ATGGTTCCAAAATC-----AATGAATATATTTGGAGCGCTTTCGGCAGATGGTAAAGGAAG	355
QY	871	ga-ggtatccgctgcgtcttggaggggaaatggttacaaacgtcatcaaaaatgtgtcttcyag	929
Db	336	GACGGAAATCCCTTCCTTTGGAGAGGAATGGCACCAATGTCATCAATCAAAATAGCTCCGAG	415
QY	930	acagctgttaaatctcttggacatgatgaacagcagaagaagatctactacagaaagaagaca	989
Db	416	ACAGCTGTGAAGTTCTGGGCTTTATGACAGATACAGAAAGTTGCTTTACCGAGAGAAAGACA	475
QY	990	a-aaataggaacatttgaagagatthattcttgttccatagtcgtgagcaactgcacagac	1048
Db	476	ACAATTAATGAGCACTTTGAGAGGTTATCTCTGTGTTCATGGCTGGAGCAACTGCTCAGAC	535
QY	1049	ttttatatatccaatatggaggttatgaaaacagagctgtgctgtatggcaaaactgtggcagta	1108
Db	536	TTTTATTATACCCCAATGAGGAGGTTTGAAAAACCCGGCTACTCTTAGCCAAATGTGCAATYA	595
QY	1109	ctctgaaatataatgatgtgccaagaagaattttgaacatgaagcttggagagctttta	1168
Db	596	CTCCGGATATACGTTTGCGCCAAAGACA-TTTGAAACACAGAGCTTTGGGCGCTTTTAA	654
QY	1169	caaaagctatgtcttcccaattta-ttaggtatcatcatccttatgcagcagaatgactgtctg	1227
Db	655	CAAGGCTACATTCGCCAATTTACGAGGACATCATTCCTTTACGAGGCGATGATCGCGTG	714
QY	1228	tgtatgagctcttgaagtccatgtgctgga-taatttgcaaaagatctgttaacc	1285
Db	715	TGTACGACTCTTTGAAAGCTTATCGGCTGAGTTACTTGTGCCAAAGACTCGCTCAACCC	773
RESULT	8		
BI962667			
LOCUS		556 bp	linear
DEFINITION		1653b05.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens	EST 23-OCT-2001
DEFINITION		cDNA 5' similar to TR:Q9UG66 Q9UG66 HYPOTHETICAL. 11.3 KD PROTEIN.	
DEFINITION		; mRNA sequence.	
ACCESSION		BI962667	
VERSION		BI962667.1	GI:16337072
KEYWORDS		EST.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;	
REFERENCE		Mammalia: Euthera: Primates: Catarrhini: Homnidae: Homo.	
REFERENCE		1 (bases 1 to 556)	
REFERENCE		Melton,D., Brown,J., Kenty,G., Permut,A., Lee,C., Kaestner,K.,	
REFERENCE		Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S.,	
REFERENCE		Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blisstein,A.,	
REFERENCE		Schmitt,L., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas	
REFERENCE		,M., Gibbons,M., McCann,R., Cole,R., Tsagarrelshvili,R., Williams,T.	
REFERENCE		, Jackson,Y. and Bowers,Y.	
REFERENCE		Endocrine Pancreas Consortium	
REFERENCE		Unpublished (2000)	
REFERENCE		Other-ESTs: 1653b05.x1	
REFERENCE		Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue	
REFERENCE		Endocrine Pancreas Consortium	
REFERENCE		Harvard University, Howard Hughes Medical Institute	
REFERENCE		Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,	
REFERENCE		MA 02138	
REFERENCE		Tel: 617-495-1812	
REFERENCE		Fax: 617-495-8557	
REFERENCE		Email: dmelton@biochem.harvard.edu	
REFERENCE		Library was constructed by Dr. Douglas Melton DNA sequencing by:	
REFERENCE		Washington University Genome Sequencing Center for information on	
REFERENCE		obtaining a clone please contact: Juliana Brown	
REFERENCE		(Brown@fas.harvard.edu)	

QY 601 cgttaccagacattggaataatccgttcttcgtgaacaattctacaggaattgacatag 660
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Db 361 CTGTTACAGACATTTGAGGAATTTATCCGTTTCTGGAAACATTTCTACAGGAATTGACATAG 420
QY 661 gggatgacttaactatctccagatgatctcagcgaagaagcaaaaaaacccgagacaatggt 720
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Db 421 GGGATGACTTAACCTATCTCCAGATGAAATTCACGGAGACGAAAAAATCCGGCAATGAT 480
QY 721 gggagcagcttttgcgagagagcat 745
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Db 481 GGAGCAGCTTTTGGCAGAGGCAAT 505
RESULT 10
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LOCUS 601645924F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4102109 5',
DEFINITION mRNA sequence.
ACCESSION BF132795
VERSION BF132795.1 GI:10971835
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 844)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHM974 row: o column: 06
High quality sequence stop: 534.
Location/Qualifiers
1. 844
FEATURES
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4102109"
/clone_lib="NIH_MGC_59"
/tissue_type="nucoepidermoid carcinoma"
/lab_host="DH10B (PI phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgccgtcgcc); Site_2: SfiI (ggcattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAGCGCGAGCGCGCACATG-3' (30)BN-3'
(where B = A, C, G, or T and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
library."
BASE COUNT 233 a 148 c 168 g 295 t
ORIGIN
Query Match 18.5%; Score 493.8; DB 10; Length 844;
Best Local Similarity 96.4%; Pred. No. 3, 4e-73;
Matches 591; Conservative 0; Mismatches 12; Indels 10; Gaps 8;
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Db 1 TCGTTTAGCCTGATTAATTAACCTTTCAACAATCCCTGGAGTACTTTTCTCTCGAAT 60
QY 1644 tgaacaagctctatggcaaaagaagctgtctttttcacaagaaggaagcgtacaa 1703

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Db 61 TGAACAAGCTCTATGCAAAAAGAGCTGATTTTTCACAAAAGGAGATGTAACAA 120
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Db 121 TGGCACTTCAAAAC-TTTGGCTTAATTAATTAATGACACAGAAAGTTCAAAATCATAGTT 179
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QY 1824 tctctgccctgaaatcgaatctgaaatgtaacatgctgctgcaacaaaatttgcttgctg 1883
Db 239 TCTCTGCCCTGAAATCCGAAATCTGAAATGACTGCTGAAACAAATTTGTTGTGAG-- 296
QY 1884 ttgagatataaatcatcaatctcttctctctctctctctctctctctctctctctctct 1943
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QY 2064 ataagtaaggttatatgctcttctctctctctctctctctctctctctctctctct 2123
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QY 2124 ggaattctcgaaggagatgatgaattatattatcttcaagtggcactttcatttta 2183
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LOCUS 601510825F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912103 5',
DEFINITION mRNA sequence.
ACCESSION BE885075
VERSION BE885075.1 GI:10333851
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 921)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHM9730 row: b column: 08
High quality sequence stop: 534.
Location/Qualifiers
1. 921
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OY	188	cgcggagacagccgcgaacgccttacgagaccctctccagcagcatcgacccgcaatgggagacg	247
Db	105	CGCCGAGCGCCGCCACACGCTACGAACGCTCTTCGCGGCGCCTTGAGACCGAATGGGGACCG	164
OY	248	agtgttgacatcggcgcgactcgcaggaggggctcgsaagacctgggcatccctctggacca	307
Db	165	CGTGTGTGACATCGGAGAGCTGCACACAGGCGCTGCAGAAACCCCTGGGCATCCCCTGGCCA	224
OY	308	ggagccgcgagagaaaatttttctaactcagygaaatgtlcaacaagaatgggaacgtgatctt	367
Db	225	GGACCGGAGGAGAAAATTTCACACTGGCGATGTCAAACAAGATGGGMACTGGATTT	284
OY	368	tgaagaatttatgaagttaaccttaagaacatgagaagaatagaattgcatltaaag	427
Db	285	TGAAATAATTATTAAGAATATACCTTAAGAACCATAGAGAAATAATGAATTATGCAATTTAAAG	344
OY	428	tttagacaaaaataatgatgtgnaaaaattgagytctcagaaatgtgcacgtctccagac	487
Db	345	TTTTGACACAAGATATATGACGGGAAATGAGAGCTTCTGAAATTTGCAAGTCTCCAGAT	404
OY	488	actggtctgactattcttcgaaacaacagcagagttgattcttccaagcatgatgttga	547
Db	405	GCTCGTTTAACTATATTTCTGAAAAACAAGCAAGCTGATTTCTTCAAGCATGACCTCGA	464
OY	548	tggagcaatgagcagtgagctggaatgaaatgagagacactctatataaccctgtac	607
Db	465	TGGGCGATGACCGGTGGACTGGATGAATGAGAGGATTAATTATTTAAACCTCGTGAC	524
OY	608	agacattgaggaatatcgcgttctcggaaacattctcaggaattgacatagggagatag	667
Db	525	AGACATGAAGAATATATTCGTTCTGGAACACACTCTACTGGAATTGACATAGAGGATAG	584
OY	668	cttaactatccagatgaattcaacggaacgagaaaaaacctcgg	712
Db	585	TTTAACTATTCCAGATGATTCACAGAGATGAGAAAAAATCAG	629
<hr/>			
RESULT	13		
LOCUS	BC894729	531 bp	mRNA linear EST 05-JUN-2001
DEFINITION	35456 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.		
ACCESSION	BC894729		
VERSION	BC894729.1 GI:14304970		
KEYWORDS	EST.		
SOURCE	pig.		
ORGANISM	Sus scrofa		
	Euarchonta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		
REFERENCE	1 (bases 1 to 531)		
AUTHORS	Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E... Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keeler,J.W.		
	Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine		
TITLE	Unpublished (2000)		
JOURNAL	Contact: Smith TPL		
COMMENT	USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@emil.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options. PCR primers FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCAGTACGACGACG Plate: 119 row: K column: 13 Seq primer: ATTTAGGTGACACTATAG.		

FEATURES	Source	Location/Qualifiers
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		/organism="Sus scrofa"
		/db_xref="taxon:9823"
		/clone_lib="MARC 1Pig"
		/tissue_type="pooled"
		/lab_host="DH10B"
		/note="Vector: pCMV SPOR6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
BASE COUNT	160 a 92 c 140 g 139 t	
ORIGIN		
Query Match	17.3%; Score 462.2; DB 10; Length 531;	
Best Local Similarity	91.9%; Pred. No. 6.8e-68;	
Matches 488;	Conservative 0; Mismatches 43; Indels 0; Gaps 0;	
QY	533 aagcatgtatgtttgattgggacaatgacagctgtgacttgaatgaatgagagactacttctt 592	
Db	1 AAGCATGTATGCTGATGGGACACATATACAGTGCATGACATGATGATGAGGAGCATCTTCT 60	
QY	593 atttaacctgttaagaagcattgagaaatttcctgtttctgaaacattctcaaggat 652	
Db	61 ATTATATCCCGTTACAGACATTGAGGAATTTATCCGTTTCGAAACATTCTACCGGTA 120	
QY	653 tgacataaggagatagcttaactatctccagatgaattcacagaaagacgaaaaaaatccgg 712	
Db	121 TGACATAGGAGACACTTAACTATTCGCGATGATGATTCACGGAAATGAAAAAGTCAGG 180	
QY	713 acaatggtggaaggaagcagcttttgccaggaaggaatgtgctgtctctcgaaagaac 772	
Db	181 ACAGTGTGGAGGCGACGCTCTTGGCGAGGAGTGTTCGCCGCCGCGCTCTCGAACAGAC 240	
QY	773 tggcccttggaaacccgtgaaatcatatgatgagtttaacggtttaaataatcgacaaaat 832	
Db	241 TGCCCCCTTGGATCCTCTGAAAGTATATGATGACAGTTCATGTTTAAATTCAGAGAAAT 300	
QY	833 gaacatacttggtgcttctcgacagatgataaagaagagatcgcgtcgtcttgag 892	
Db	301 GAACATATATGCTGGCTTTCGACAGATGCTGAAAGAAAGAGGAGATCCCTCCTTTGGAG 360	
QY	893 gggaaatggtacaacgctcatcaaaaattgtcttcgtgagacagctgtgtaattcttggcata 952	
Db	361 AGGAATATGTCACAAATGTCATTTAAATTCGCCCTGAGACAGCTGTTAAGTTCTGGGCA 420	
QY	953 tgaacagtaagaagaagttacttacttcgaagaagaagaaaaaataagaacattgaagatt 1012	
Db	421 TGAACAGTACAAAGAAATTTGCTTACTGAGAGAAAGCAAAAAGTAGGAACTTTTGAAGATT 480	
QY	1013 tattctgtgtccatgctgctgagcaacgcacagccttataatcaat 1063	
Db	481 TATTTCGTGTTCCATAGGCTGGAGCAACGCAAACTTTTATTATCTAT 531	
RESULT 14		
LOCUS	BG894680	529 bp mRNA linear EST 05-JUN-2001
DEFINITION	353388 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.	
ACCESSION	BG894680	
VERSION	BG894680.1	GI:14304921
KEYWORDS	EST.	
SOURCE	pig.	
ORGANISM	Sus scrofa	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.	
REFERENCE	1 (bases 1 to 529)	
AUTHORS	Fehrenking,S.C., Fekking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keel,J.W.	
TITLE	Design and use of two pooled tissue normalized cDNA libraries for	
JOURNAL	EST discovery in swine	
	Unpublished (2000)	


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QY 562 tggactggaaatggagagactactcttatttaacctgttcagacattgaggaa 621
    |||||
Db 416 TGGACTGGAAATGAATGAGAGGATTTACTTTTATTTAACCTGTGACAGACTTGAGGAA 475
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QY 622 ttatcgcttctcggaacattctacaggaattgacatagggatagcttaactatccag 681
    |||||
Db 476 TTATCCGTTTCTGGAACACTCTACTGGAATTGACATAGGGGATGTTTAACTATTCCAG 535
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QY 682 atgaattcaaggaaagcaaaaaaatc-cggacaatggtggagcaagctttggcagga 740
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Db 536 ATGAATTCACAGAAAGATGAGAAAAATCACGACAGTGTGTGAGGACGCTCTGCGCAGGA 595
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QY 741 ggcattgctgtgctgtctcgaacaagcactgcccttggacgctcgaataatcatg 800
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Db 596 GGTGTGGCGGGCGCGCTCTCTAGAACGAGCAC--GTCCTTGGATCCGCTCAAGTCAATG 653
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QY 801 atgcaggttcaaggttcaaatcagacaaat 832
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